

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2004, 09:06:30 ; Search time 54 Seconds
(without alignments)
31.394 Million cell updates/sec

Title: US-10-024-329-2

Perfect score: 35

Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	2	AAR43703 HIV-1 gp1
2	35	100.0	6	2	AAR68698 Katinger
3	35	100.0	6	2	AAR92010 HIV-1 gp4
4	35	100.0	6	2	AAR25868 HIV-1 gp4
5	35	100.0	6	2	AAW53143 HIV gp41
6	35	100.0	6	2	AAW67384 Katinger
7	35	100.0	6	2	AAW99905 HIV-1 vac
8	35	100.0	6	2	AAW39717 HIV-1 chim
9	35	100.0	6	3	AAW57748 Peptide a
10	35	100.0	6	3	AAW24104 HIV-1 gp4
11	35	100.0	6	4	AAW63933 Amino aci
12	35	100.0	6	4	AAW92333 Virus rel
13	35	100.0	6	4	AAW65282 HIV-1 iso
14	35	100.0	6	4	AAW98918 HIV epito
15	35	100.0	6	4	AAW63974 Amino aci
16	35	100.0	6	5	ABW07403 HIV-1 gp4
17	35	100.0	6	5	ABW14868 HIV epito
18	35	100.0	6	6	ABR39670 HIV-1 gp4
19	35	100.0	6	7	ABR62944 HIV-1 vir
20	35	100.0	6	7	ADC79307 HIV-1 gp4
21	35	100.0	7	2	AAW71631 HIV-1 gp4
22	35	100.0	7	2	AAW94444 HIV-1 gp4
23	35	100.0	7	2	AAW25897 Peptide c
24	35	100.0	7	2	AAW67413 HIV-1 gp4
25	35	100.0	7	2	AAW99911 HIV-1 vac

26	35	100.0	7	2	AAW39741	AAW39741 HIV1 chim
27	35	100.0	7	3	AAB29401	AAB29401 HIV-1 env
28	35	100.0	7	4	AAU70190	AAU70190 P3 peptid
29	35	100.0	7	4	AAG63975	AAG63975 Amino aci
30	35	100.0	7	5	AAU80301	AAU80301 HIV-1 can
31	35	100.0	7	5	AAU99586	AAU99586 Epitope o
32	35	100.0	7	5	AAU97480	AAU97480 HIV-1 inf
33	35	100.0	7	6	ABR39671	ABR39671 HIV-1 gp4
34	35	100.0	7	7	ABR62950	ABR62950 HIV-1 vir
35	35	100.0	7	7	ABR62947	ABR62947 HIV-1 vir
36	35	100.0	8	2	AAW71632	AAW71632 MN-HIV gp4
37	35	100.0	8	2	AAW05254	AAW05254 MN-HIV gp
38	35	100.0	8	4	ABP12065	ABP12065 HIV A02 s
39	35	100.0	8	4	ABP12063	ABP12063 HIV A02 s
40	35	100.0	8	4	ABP15180	ABP15180 HIV A24 s
41	35	100.0	8	4	ABP20177	ABP20177 HIV A03 m
42	35	100.0	8	5	AAU97481	AAU97481 HIV-1 inf
43	35	100.0	8	7	ABR62953	ABR62953 HIV-1 vir
44	35	100.0	9	2	AAW71637	AAW71637 Immunizat
45	35	100.0	9	2	AAW99914	AAW99914 HIV-1 vac
46	35	100.0	9	4	ABP20096	ABP20096 HIV A03 m
47	35	100.0	9	4	ABP15290	ABP15290 HIV A24 s
48	35	100.0	9	4	ABP12211	ABP12211 HIV A02 s
49	35	100.0	9	4	ABP18573	ABP18573 HIV B62 s
50	35	100.0	10	3	AAB38721	AAB38721 HIV-1 pep
51	35	100.0	10	3	AAB38723	AAB38723 HIV-1 pep
52	35	100.0	10	3	AAB38722	AAB38722 HIV-1 pep
53	35	100.0	10	4	ABP12372	ABP12372 HIV A02 s
54	35	100.0	10	4	ABP15481	ABP15481 HIV A24 s
55	35	100.0	10	4	ABP11618	ABP11618 HIV A01 s
56	35	100.0	10	4	ABP15479	ABP15479 HIV A24 s
57	35	100.0	10	4	ABP11616	ABP11616 HIV A01 s
58	35	100.0	10	4	ABP15483	ABP15483 HIV A24 s
59	35	100.0	10	4	ABP15393	ABP15393 HIV A24 s
60	35	100.0	10	5	AAU87761	AAU87761 HIV-1 epi
61	35	100.0	10	5	AAU93905	AAU93905 HIV-1 gp4
62	35	100.0	10	6	ABU70159	ABU70159 Human imm
63	35	100.0	10	6	ABU69713	ABU69713 Human imm
64	35	100.0	10	6	ABU70138	ABU70138 Human imm
65	35	100.0	10	6	ABU70086	ABU70086 Human imm
66	35	100.0	10	7	ADD96692	ADD96692 HIV-1 cro
67	35	100.0	10	7	ADD96619	ADD96619 HIV-1 cro
68	35	100.0	10	7	ADD96246	ADD96246 HIV-1 cro
69	35	100.0	10	7	ADD96671	ADD96671 HIV-1 cro
70	35	100.0	11	2	AAW99913	AAW99913 HIV-1 vac
71	35	100.0	11	3	AAW38671	AAW38671 HIV-1 pep
72	35	100.0	11	4	ABP18579	ABP18579 HIV B62 s
73	35	100.0	11	4	ABP18554	ABP18554 HIV B62 s
74	35	100.0	11	4	ABP12499	ABP12499 HIV A02 s
75	35	100.0	11	4	ABP12498	ABP12498 HIV A02 s
76	35	100.0	12	2	AAW64374	AAW64374 DP-178 ho
77	35	100.0	12	2	AAW99912	AAW99912 HIV-1 vac
78	35	100.0	12	2	AAW31961	AAW31961 Side-chai
79	35	100.0	12	3	AAW88866	AAW88866 Core poly
80	35	100.0	12	3	AAW14647	AAW14647 HIV-1 iso
81	35	100.0	12	3	AAW52664	AAW52664 T20/DP178
82	35	100.0	12	3	AAW52709	AAW52709 T20/DP178
83	35	100.0	12	4	AAW54911	AAW54911 Anti-HIV
84	35	100.0	12	4	AAW77221	AAW77221 Core poly
85	35	100.0	12	4	ABW00225	ABW00225 Viral DP1
86	35	100.0	12	4	ABW01692	ABW01692 Viral cor
87	35	100.0	12	4	AAU12774	AAU12774 DP178-lik
88	35	100.0	12	5	AAE011712	AAE011712 Hybrid po
89	35	100.0	12	6	ABR39672	ABR39672 HIV-1 gp4
90	35	100.0	12	7	ABR62958	ABR62958 Anti-HIV-
91	35	100.0	13	2	AAW71639	AAW71639 Chimeric
92	35	100.0	13	2	AAW64375	AAW64375 DP-178 ho
93	35	100.0	13	2	AAW92001	AAW92001 HIV-1 gp4
94	35	100.0	13	2	AAW31962	AAW31962 Side-chai
95	35	100.0	13	3	AAW89170	AAW89170 Core poly
96	35	100.0	13	3	AAW88910	AAW88910 Core poly
97	35	100.0	13	3	AAW88865	AAW88865 Core poly
98	35	100.0	13	3	AAW89169	AAW89169 Core poly

99 35 100.0 13 3 AAY88907 Core poly
100 35 100.0 13 3 AAY88908 Core poly
101 35 100.0 13 3 AAY88909 Core poly
102 35 100.0 13 3 AAB14606 HIV-1 iso
103 35 100.0 13 3 AAB14648 HIV-1 iso
104 35 100.0 13 3 AAB52708 T20/DP178
105 35 100.0 13 3 AAB52665 T20/DP178
106 35 100.0 13 4 AAB54912 Anti-HIV
107 35 100.0 13 4 AAB77220 Core poly
108 35 100.0 13 4 AAB77265 Core poly
109 35 100.0 13 4 AAB77523 Core poly
110 35 100.0 13 4 AAB77524 Core poly
111 35 100.0 13 4 AAB77264 Core poly
112 35 100.0 13 4 AAB77263 Core poly
113 35 100.0 13 4 AAU70189 HIV viral
114 35 100.0 13 4 ABB00527 Viral DP1
115 35 100.0 13 4 ABB01742 Viral cor
116 35 100.0 13 4 ABB00266 Viral DP1
117 35 100.0 13 4 ABB00269 Viral DP1
118 35 100.0 13 4 ABB00224 Viral DP1
119 35 100.0 13 4 ABB00267 Viral DP1
120 35 100.0 13 4 ABB02004 Viral cor
121 35 100.0 13 4 ABB02003 Viral cor
122 35 100.0 13 4 ABB01743 Viral cor
123 35 100.0 13 4 ABB01691 Viral cor
124 35 100.0 13 4 ABB01740 Viral cor
125 35 100.0 13 4 ABB00528 Viral DP1
126 35 100.0 13 4 ABB01741 Viral cor
127 35 100.0 13 4 ABB01741 Viral cor
128 35 100.0 13 4 AAU113076
129 35 100.0 13 4 AAU12816
130 35 100.0 13 4 AAU12818
131 35 100.0 13 4 AAU12815
132 35 100.0 13 4 AAU12817
133 35 100.0 13 4 AAU13077
134 35 100.0 13 4 AAU12773 DP178-lik
135 35 100.0 13 4 AAU12773 DP178-lik
136 35 100.0 13 5 ADE01762 Hybrid po
137 35 100.0 13 5 ADE01711 Hybrid po
138 35 100.0 13 5 ADE01760 Hybrid po
139 35 100.0 13 5 ADE01763 Hybrid po
140 35 100.0 13 5 ADE02023 Hybrid po
141 35 100.0 13 5 ADE01761 Hybrid po
142 35 100.0 13 5 ADE02024 Hybrid po
143 35 100.0 13 6 ABO10326 HIV-1 BRU
144 35 100.0 13 6 ABO10328 HIV-1 BRU
145 35 100.0 13 6 ABO10327 HIV-1 BRU
146 35 100.0 13 6 ABO10329 HIV-1 BRU
147 35 100.0 13 6 ABO10325 HIV-1 BRU
148 35 100.0 14 1 AAP71141 Anti-HIV
149 35 100.0 14 2 AAR64376 DP-178 ho
150 35 100.0 14 2 AAR64376 DP-178 ho
151 35 100.0 14 3 AAW99915 HIV-1 vac
152 35 100.0 14 3 AAY88864 Core poly
153 35 100.0 14 3 AAB14649 HIV-1 iso
154 35 100.0 14 3 AAB52666 T20/DP178
155 35 100.0 14 3 AAB52707 T20/DP178
156 35 100.0 14 4 AAB54913 Anti-HIV
157 35 100.0 14 4 ABO101690 Viral cor
158 35 100.0 14 4 ABO101702 Viral cor
159 35 100.0 14 5 AAU87762 HIV-1 epi
160 35 100.0 14 5 AAU93906 HIV-1 gp4
161 35 100.0 14 5 ABO101722 Hybrid po
162 35 100.0 15 1 AAP90238 Antigenic
163 35 100.0 15 2 AAR68722 B cell ep
164 35 100.0 15 2 AAR68688 CLTB-96 B
165 35 100.0 15 2 AAR64377 DP-178 ho
166 35 100.0 15 2 AAW32891 HIV envel
167 35 100.0 15 2 AAW25892 Gp41 pept
168 35 100.0 15 2 AAW25858 HIV-1 T/B
169 35 100.0 15 2 AAW67374 HIV-1 pep
170 35 100.0 15 2 AAW67408 HIV-1 GP4
171 35 100.0 15 2 AAW99908 HIV-1 vac

172 35 100.0 15 2 AAW99910 HIV-1 vac
173 35 100.0 15 2 AAY39737 HIV1 chim
174 35 100.0 15 2 AAY39707 HIV1 chim
175 35 100.0 15 3 AAY88863 Core poly
176 35 100.0 15 3 AAY89154 Core poly
177 35 100.0 15 3 AAY89014 Core poly
178 35 100.0 15 3 AAY89152 Core poly
179 35 100.0 15 3 AAY89381 Core poly
180 35 100.0 15 3 AAY89012 Core poly
181 35 100.0 15 3 AAY89013 Core poly
182 35 100.0 15 3 AAY89153 Core poly
183 35 100.0 15 3 AAB14650 HIV-1 iso
184 35 100.0 15 3 AAB52706 T20/DP178
185 35 100.0 15 3 AAB52667 T20/DP178
186 35 100.0 15 4 AAB54914 Anti-HIV
187 35 100.0 15 4 AAB77369 Core poly
188 35 100.0 15 4 AAB77508 Core poly
189 35 100.0 15 4 AAB77506 Core poly
190 35 100.0 15 4 AAB77367 Core poly
191 35 100.0 15 4 AAB77219 Core poly
192 35 100.0 15 4 AAB77368 Core poly
193 35 100.0 15 4 AAB77507 Core poly
194 35 100.0 15 4 ABB00373 Viral DP1
195 35 100.0 15 4 ABB00511 Viral DP1
196 35 100.0 15 4 ABB00512 Viral DP1
197 35 100.0 15 4 ABB00371 Viral DP1
198 35 100.0 15 4 ABB02265 Viral cor
199 35 100.0 15 4 ABB01847 Viral cor
200 35 100.0 15 4 ABB01986 Viral cor
201 35 100.0 15 4 ABB00789 Viral DP1
202 35 100.0 15 4 ABB01845 Viral cor
203 35 100.0 15 4 ABB00372 Viral DP1
204 35 100.0 15 4 ABB01689 Viral cor
205 35 100.0 15 4 ABB01846 Viral cor
206 35 100.0 15 4 ABB01988 Viral cor
207 35 100.0 15 4 ABB00510 Viral DP1
208 35 100.0 15 4 ABB00223 Viral DP1
209 35 100.0 15 4 ABB01987 Viral cor
210 35 100.0 15 4 ABP24896 HIV DR 3a
211 35 100.0 15 4 AAU12920 DP178-lik
212 35 100.0 15 4 AAU13061 DP178-lik
213 35 100.0 15 4 AAU12921 DP178-lik
214 35 100.0 15 4 AAU13059 DP178-lik
215 35 100.0 15 4 AAU12922 DP178-lik
216 35 100.0 15 4 AAU13060 DP178-lik
217 35 100.0 15 4 AAU12772 DP178-lik
218 35 100.0 15 4 AAU12772 DP178-lik
219 35 100.0 15 5 ABG68680 HIV-1 P21
220 35 100.0 15 5 ADE02007 Hybrid po
221 35 100.0 15 5 ADE01865 Hybrid po
222 35 100.0 15 5 ADE02007 Hybrid po
223 35 100.0 15 5 ADE01710 Hybrid po
224 35 100.0 15 5 ADE01867 Hybrid po
225 35 100.0 15 5 ADE02006 Hybrid po
226 35 100.0 15 5 ADE01866 Hybrid po
227 35 100.0 15 5 ADE02285 Hybrid po
228 35 100.0 15 5 ADE02285 Hybrid po
229 35 100.0 15 6 ABO10322 HIV-1 BRU
230 35 100.0 15 6 ABO10324 HIV-1 BRU
231 35 100.0 15 6 ABO10323 HIV-1 BRU
232 35 100.0 16 2 AAR64378 DP-178 ho
233 35 100.0 16 3 AAY88862 Core poly
234 35 100.0 16 3 AAB14651 HIV-1 iso
235 35 100.0 16 3 AAB52668 T20/DP178
236 35 100.0 16 3 AAB52705 T20/DP178
237 35 100.0 16 4 AAB54915 Anti-HIV
238 35 100.0 16 4 AAB77218 Core poly
239 35 100.0 16 4 ABB01688 Viral cor
240 35 100.0 16 4 ABB00222 Viral DP1
241 35 100.0 16 4 AAU12771 DP178-lik
242 35 100.0 16 4 AAU12771 DP178-lik
243 35 100.0 17 5 AAR93644 HIV princ
244 35 100.0 17 2 AAR93643 HIV princ

245	35	100.0	17	2	AAR68690	Aar68690	CLTB-97A	318	35	100.0	20	4	AAB77062	Aab77062	Core poly
246	35	100.0	17	2	AAR64379	Aar64379	DP-178 ho	319	35	100.0	20	4	AAB77783	Aab77783	Core poly
247	35	100.0	17	2	AAW19023	Aaw19023	HIV envel	320	35	100.0	20	4	ABB00790	Abb00790	Viral DP1
248	35	100.0	17	2	AAW25860	Aaw25860	HIV-1 T/B	321	35	100.0	20	4	ABB02266	Abb02266	Viral cor
249	35	100.0	17	2	AAW67376	Aaw67376	HIV-1 pep	322	35	100.0	20	4	ABB01531	Abb01531	Viral cor
250	35	100.0	17	2	AAW99909	Aaw99909	HIV-1 vac	323	35	100.0	20	4	ABB00066	Abb00066	Viral DP1
251	35	100.0	17	2	AAW39709	Aaw39709	HIV1 chim	324	35	100.0	20	4	AAU12615	Aau12615	DP178-lik
252	35	100.0	17	2	AAW31972	Aaw31972	Side-chai	325	35	100.0	20	4	AAU13336	Aau13336	DP178-lik
253	35	100.0	17	3	AAW88861	Aaw88861	Core poly	326	35	100.0	20	5	AAO18824	Aao18824	HIV gp41
254	35	100.0	17	3	AAW14652	Aaw14652	Core poly	327	35	100.0	20	5	AAO1551	Aao1551	Hybrid po
255	35	100.0	17	3	AAW52704	Aaw52704	T20/DP178	328	35	100.0	20	5	AAO22286	Aao22286	Hybrid po
256	35	100.0	17	3	AAW52669	Aaw52669	T20/DP178	329	35	100.0	20	5	ABR39655	Abr39655	HIV-1 gp4
257	35	100.0	17	4	AAW54916	Aaw54916	Anti-HIV	330	35	100.0	20	6	ABR39673	Abr39673	HIV-1 gp4
258	35	100.0	17	4	AAW77217	Aaw77217	Core poly	331	35	100.0	21	2	AAR13068	Aar13068	HIV647 fu
259	35	100.0	17	4	ABBO1687	Abbo1687	Vital cor	332	35	100.0	21	2	AAR64383	Aar64383	DP-178 ho
260	35	100.0	17	4	ABBO0221	Abbo0221	Vital DP1	333	35	100.0	21	2	AAW13968	Aaw13968	Side-chai
261	35	100.0	17	4	AAW63978	Aaw63978	Amino aci	334	35	100.0	21	3	AAW89842	Aaw89842	Core poly
262	35	100.0	17	4	AAU12770	Aau12770	DP178-lik	335	35	100.0	21	3	AAW89843	Aaw89843	Core poly
263	35	100.0	17	5	AAE01708	Aae01708	Hybrid po	336	35	100.0	21	3	AAW89698	Aaw89698	Core poly
264	35	100.0	18	2	AAR68686	Aar68686	CLTB-94 B	337	35	100.0	21	3	AAW89699	Aaw89699	Core poly
265	35	100.0	18	2	AAR64380	Aar64380	DP-178 ho	338	35	100.0	21	3	AAW14656	Aaw14656	HIV-1 iso
266	35	100.0	18	2	AAW25856	Aaw25856	HIV-1 T/B	339	35	100.0	21	3	AAW52673	Aaw52673	T20/DP178
267	35	100.0	18	2	AAW67372	Aaw67372	HIV-1 pep	340	35	100.0	21	3	AAW52700	Aaw52700	T20/DP178
268	35	100.0	18	2	AAW99907	Aaw99907	HIV-1 vac	341	35	100.0	21	4	AAW54920	Aaw54920	Anti-HIV
269	35	100.0	18	2	AAW39705	Aaw39705	HIV1 chim	342	35	100.0	21	4	AAW78244	Aaw78244	Core poly
270	35	100.0	18	2	AAW31970	Aaw31970	Side-chai	343	35	100.0	21	4	AAW78100	Aaw78100	Core poly
271	35	100.0	18	3	AAW88747	Aaw88747	Core poly	344	35	100.0	21	4	AAW78099	Aaw78099	Core poly
272	35	100.0	18	3	AAW88653	Aaw88653	Core poly	345	35	100.0	21	4	AAW78243	Aaw78243	Core poly
273	35	100.0	18	3	AAW88706	Aaw88706	Core poly	346	35	100.0	21	4	ABB01250	Abb01250	Vital DP1
274	35	100.0	18	3	AAW14653	Aaw14653	HIV-1 iso	347	35	100.0	21	4	ABB02555	Abb02555	Vital cor
275	35	100.0	18	3	AAW52670	Aaw52670	T20/DP178	348	35	100.0	21	4	ABB02556	Abb02556	Vital cor
276	35	100.0	18	3	AAW52703	Aaw52703	T20/DP178	349	35	100.0	21	4	ABB02835	Abb02835	Vital cor
277	35	100.0	18	4	AAW54917	Aaw54917	Anti-HIV	350	35	100.0	21	4	ABB01251	Abb01251	Vital DP1
278	35	100.0	18	4	AAW77102	Aaw77102	Core poly	351	35	100.0	21	4	ABB01107	Abb01107	Vital DP1
279	35	100.0	18	4	AAW77008	Aaw77008	Core poly	352	35	100.0	21	4	ABB01106	Abb01106	Vital DP1
280	35	100.0	18	4	AAW77061	Aaw77061	Core poly	353	35	100.0	21	4	AAU13653	Aau13653	DP178-lik
281	35	100.0	18	4	ABB00106	Abb00106	Vital DP1	354	35	100.0	21	4	AAU13796	Aau13796	DP178-lik
282	35	100.0	18	4	ABB00012	Abb00012	HIV-1 gp4	355	35	100.0	21	4	AAU13797	Aau13797	DP178-lik
283	35	100.0	18	4	ABB02923	Abb02923	Vital cor	356	35	100.0	21	4	AAU13652	Aau13652	DP178-lik
284	35	100.0	18	4	ABB01530	Abb01530	Vital cor	357	35	100.0	21	5	ADE02576	Ade02576	Hybrid po
285	35	100.0	18	4	ABB01571	Abb01571	Vital cor	358	35	100.0	21	5	ADE02575	Ade02575	Hybrid po
286	35	100.0	18	4	ABB00065	Abb00065	Vital DP1	359	35	100.0	21	5	ADE02855	Ade02855	Hybrid po
287	35	100.0	18	4	ABB01476	Abb01476	HIV-1 tra	360	35	100.0	21	5	ADE02856	Ade02856	Hybrid po
288	35	100.0	18	4	AAU12655	Aau12655	DP178-lik	361	35	100.0	22	2	AAR64384	Aar64384	DP-178 ho
289	35	100.0	18	4	AAU12561	Aau12561	DP178-lik	362	35	100.0	22	3	AAW14657	Aaw14657	HIV-1 iso
290	35	100.0	18	4	AAU12614	Aau12614	DP178-lik	363	35	100.0	22	3	AAW52674	Aaw52674	T20/DP178
291	35	100.0	18	5	ADE01496	Ade01496	Hybrid po	364	35	100.0	22	3	AAW52699	Aaw52699	T20/DP178
292	35	100.0	18	5	ADE01591	Ade01591	Hybrid po	365	35	100.0	22	4	AAW54921	Aaw54921	Anti-HIV
293	35	100.0	18	5	ADE01550	Ade01550	Hybrid po	366	35	100.0	23	1	AAW82469	Aaw82469	Peptide c
294	35	100.0	19	2	AAW64381	Aaw64381	DP-178 ho	367	35	100.0	23	2	AAR68696	Aar68696	T1/Kating
295	35	100.0	19	2	AAW31963	Aaw31963	Side-chai	368	35	100.0	23	2	AAR64385	Aar64385	DP-178 ho
296	35	100.0	19	3	AAW14654	Aaw14654	HIV-1 iso	369	35	100.0	23	2	AAW07974	Aaw07974	HIV pepti
297	35	100.0	19	3	AAW52702	Aaw52702	T20/DP178	370	35	100.0	23	2	AAW25866	Aaw25866	HIV-1 T/B
298	35	100.0	19	3	AAW52671	Aaw52671	T20/DP178	371	35	100.0	23	2	AAW67382	Aaw67382	HIV-1 pep
299	35	100.0	19	4	AAW54918	Aaw54918	Anti-HIV	372	35	100.0	23	2	AAW99986	Aaw99986	HIV-1 vac
300	35	100.0	20	2	AAW03896	Aaw03896	HIV-antib	373	35	100.0	23	2	AAW39715	Aaw39715	HIV1 chim
301	35	100.0	20	2	AAR68684	Aar68684	CLTB-92A	374	35	100.0	23	3	AAW88708	Aaw88708	Core poly
302	35	100.0	20	2	AAR64382	Aar64382	DP-178 ho	375	35	100.0	23	3	AAW14658	Aaw14658	HIV-1 iso
303	35	100.0	20	2	AAW08065	Aaw08065	HIV pepti	376	35	100.0	23	3	AAW52698	Aaw52698	T20/DP178
304	35	100.0	20	2	AAW08066	Aaw08066	HIV pepti	377	35	100.0	23	3	AAW52675	Aaw52675	T20/DP178
305	35	100.0	20	2	AAW07920	Aaw07920	gp41 pept	378	35	100.0	23	4	AAW54922	Aaw54922	Anti-HIV
306	35	100.0	20	2	AAW25854	Aaw25854	HIV-1 T/B	379	35	100.0	23	4	AAW77063	Aaw77063	Core poly
307	35	100.0	20	2	AAW67370	Aaw67370	HIV-1 pep	380	35	100.0	23	4	ABB01532	Abb01532	Vital cor
308	35	100.0	20	2	AAW99906	Aaw99906	HIV-1 vac	381	35	100.0	23	4	ABB00067	Abb00067	Vital DP1
309	35	100.0	20	2	AAW39703	Aaw39703	HIV1 chim	382	35	100.0	23	4	AAU12616	Aau12616	DP178-lik
310	35	100.0	20	2	AAW31969	Aaw31969	Side-chai	383	35	100.0	23	5	AAO18823	Aao18823	HIV gp41
311	35	100.0	20	2	AAW31958	Aaw31958	Side-chai	384	35	100.0	23	5	AAO19396	Aao19396	Chemical
312	35	100.0	20	3	AAW88707	Aaw88707	Core poly	385	35	100.0	23	5	ADE01552	Ade01552	Hybrid po
313	35	100.0	20	3	AAW89382	Aaw89382	Core poly	386	35	100.0	23	6	ABR39666	Abr39666	HIV-1 gp4
314	35	100.0	20	3	AAW14655	Aaw14655	HIV-1 iso	387	35	100.0	24	2	AAW68694	Aaw68694	P24E/CLTB
315	35	100.0	20	3	AAW52672	Aaw52672	T20/DP178	388	35	100.0	24	2	AAR64386	Aar64386	DP-178 ho
316	35	100.0	20	3	AAW52701	Aaw52701	T20/DP178	389	35	100.0	24	2	AAW19052	Aaw19052	GHT1-Sp60
317	35	100.0	20	4	AAW54919	Aaw54919	Anti-HIV	390	35	100.0	24	2	AAW25864	Aaw25864	HIV-1 T/B

391	35	100.0	24	2	AAW67380	AAW67380 HIV-1 pep	464	35	100.0	28	4	ABB01704	Abb01704 Viral cor
392	35	100.0	24	2	AAW99984	AAW99984 HIV-1 vac	465	35	100.0	28	4	ABB01705	Abb01705 Viral cor
393	35	100.0	24	2	AAW99984	AAW99984 HIV-1 vac	466	35	100.0	28	4	ABB00379	Abb00379 Viral DPl
394	35	100.0	24	3	AAW93713	AAW93713 HIV1 chlm	467	35	100.0	28	4	ABB01853	Abb01853 Viral cor
395	35	100.0	24	3	AAW89379	AAW89379 Core poly	468	35	100.0	28	4	ABB00376	Abb00376 Viral DPl
396	35	100.0	24	3	AAW89378	AAW89378 Core poly	469	35	100.0	28	4	ABB00376	Abb00376 Viral cor
397	35	100.0	24	3	AAW89378	AAW89378 Core poly	470	35	100.0	28	4	ABB00376	Abb00376 Viral cor
398	35	100.0	24	3	AAW89378	AAW89378 Core poly	471	35	100.0	28	4	ABB00376	Abb00376 Viral cor
399	35	100.0	24	3	AAW89378	AAW89378 Core poly	472	35	100.0	28	4	ABB00376	Abb00376 Viral cor
400	35	100.0	24	3	AAW89378	AAW89378 Core poly	473	35	100.0	28	4	ABB00376	Abb00376 Viral cor
401	35	100.0	24	3	AAW89378	AAW89378 Core poly	474	35	100.0	28	4	ABB00376	Abb00376 Viral cor
402	35	100.0	24	3	AAW89378	AAW89378 Core poly	475	35	100.0	28	4	ABB00376	Abb00376 Viral cor
403	35	100.0	24	3	AAW89378	AAW89378 Core poly	476	35	100.0	28	4	ABB00376	Abb00376 Viral cor
404	35	100.0	24	3	AAW89378	AAW89378 Core poly	477	35	100.0	28	4	ABB00376	Abb00376 Viral cor
405	35	100.0	24	3	AAW89378	AAW89378 Core poly	478	35	100.0	28	4	ABB00376	Abb00376 Viral cor
406	35	100.0	24	3	AAW89378	AAW89378 Core poly	479	35	100.0	28	4	ABB00376	Abb00376 Viral cor
407	35	100.0	24	3	AAW89378	AAW89378 Core poly	480	35	100.0	28	4	ABB00376	Abb00376 Viral cor
408	35	100.0	24	3	AAW89378	AAW89378 Core poly	481	35	100.0	28	4	ABB00376	Abb00376 Viral cor
409	35	100.0	24	3	AAW89378	AAW89378 Core poly	482	35	100.0	28	4	ABB00376	Abb00376 Viral cor
410	35	100.0	24	3	AAW89378	AAW89378 Core poly	483	35	100.0	28	4	ABB00376	Abb00376 Viral cor
411	35	100.0	24	3	AAW89378	AAW89378 Core poly	484	35	100.0	28	4	ABB00376	Abb00376 Viral cor
412	35	100.0	24	3	AAW89378	AAW89378 Core poly	485	35	100.0	28	4	ABB00376	Abb00376 Viral cor
413	35	100.0	24	3	AAW89378	AAW89378 Core poly	486	35	100.0	28	4	ABB00376	Abb00376 Viral cor
414	35	100.0	24	3	AAW89378	AAW89378 Core poly	487	35	100.0	28	4	ABB00376	Abb00376 Viral cor
415	35	100.0	24	3	AAW89378	AAW89378 Core poly	488	35	100.0	28	4	ABB00376	Abb00376 Viral cor
416	35	100.0	24	3	AAW89378	AAW89378 Core poly	489	35	100.0	28	4	ABB00376	Abb00376 Viral cor
417	35	100.0	24	3	AAW89378	AAW89378 Core poly	490	35	100.0	28	4	ABB00376	Abb00376 Viral cor
418	35	100.0	24	3	AAW89378	AAW89378 Core poly	491	35	100.0	28	4	ABB00376	Abb00376 Viral cor
419	35	100.0	24	3	AAW89378	AAW89378 Core poly	492	35	100.0	28	4	ABB00376	Abb00376 Viral cor
420	35	100.0	24	3	AAW89378	AAW89378 Core poly	493	35	100.0	28	4	ABB00376	Abb00376 Viral cor
421	35	100.0	24	3	AAW89378	AAW89378 Core poly	494	35	100.0	28	4	ABB00376	Abb00376 Viral cor
422	35	100.0	24	3	AAW89378	AAW89378 Core poly	495	35	100.0	28	4	ABB00376	Abb00376 Viral cor
423	35	100.0	24	3	AAW89378	AAW89378 Core poly	496	35	100.0	28	4	ABB00376	Abb00376 Viral cor
424	35	100.0	24	3	AAW89378	AAW89378 Core poly	497	35	100.0	28	4	ABB00376	Abb00376 Viral cor
425	35	100.0	24	3	AAW89378	AAW89378 Core poly	498	35	100.0	28	4	ABB00376	Abb00376 Viral cor
426	35	100.0	24	3	AAW89378	AAW89378 Core poly	499	35	100.0	28	4	ABB00376	Abb00376 Viral cor
427	35	100.0	24	3	AAW89378	AAW89378 Core poly	500	35	100.0	28	4	ABB00376	Abb00376 Viral cor
428	35	100.0	24	3	AAW89378	AAW89378 Core poly							
429	35	100.0	24	3	AAW89378	AAW89378 Core poly							
430	35	100.0	24	3	AAW89378	AAW89378 Core poly							
431	35	100.0	24	3	AAW89378	AAW89378 Core poly							
432	35	100.0	24	3	AAW89378	AAW89378 Core poly							
433	35	100.0	24	3	AAW89378	AAW89378 Core poly							
434	35	100.0	24	3	AAW89378	AAW89378 Core poly							
435	35	100.0	24	3	AAW89378	AAW89378 Core poly							
436	35	100.0	24	3	AAW89378	AAW89378 Core poly							
437	35	100.0	24	3	AAW89378	AAW89378 Core poly							
438	35	100.0	24	3	AAW89378	AAW89378 Core poly							
439	35	100.0	24	3	AAW89378	AAW89378 Core poly							
440	35	100.0	24	3	AAW89378	AAW89378 Core poly							
441	35	100.0	24	3	AAW89378	AAW89378 Core poly							
442	35	100.0	24	3	AAW89378	AAW89378 Core poly							
443	35	100.0	24	3	AAW89378	AAW89378 Core poly							
444	35	100.0	24	3	AAW89378	AAW89378 Core poly							
445	35	100.0	24	3	AAW89378	AAW89378 Core poly							
446	35	100.0	24	3	AAW89378	AAW89378 Core poly							
447	35	100.0	24	3	AAW89378	AAW89378 Core poly							
448	35	100.0	24	3	AAW89378	AAW89378 Core poly							
449	35	100.0	24	3	AAW89378	AAW89378 Core poly							
450	35	100.0	24	3	AAW89378	AAW89378 Core poly							
451	35	100.0	24	3	AAW89378	AAW89378 Core poly							
452	35	100.0	24	3	AAW89378	AAW89378 Core poly							
453	35	100.0	24	3	AAW89378	AAW89378 Core poly							
454	35	100.0	24	3	AAW89378	AAW89378 Core poly							
455	35	100.0	24	3	AAW89378	AAW89378 Core poly							
456	35	100.0	24	3	AAW89378	AAW89378 Core poly							
457	35	100.0	24	3	AAW89378	AAW89378 Core poly							
458	35	100.0	24	3	AAW89378	AAW89378 Core poly							
459	35	100.0	24	3	AAW89378	AAW89378 Core poly							
460	35	100.0	24	3	AAW89378	AAW89378 Core poly							
461	35	100.0	24	3	AAW89378	AAW89378 Core poly							
462	35	100.0	24	3	AAW89378	AAW89378 Core poly							
463	35	100.0	24	3	AAW89378	AAW89378 Core poly							

ALIGNMENTS

RESULT 1

AAW67380
ID AAW67380 standard; peptide; 6 AA.

XX AAW67380;
AC AAW67380;
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 10-AUG-1995 (first entry)

XX HIV-1 gp160 epitope, residues 662-667, from isolate BH10.

DE Epitope; gp160; strain; isolate; HIV-1; antibody; monoclonal antibody;
KW 2F5; vaccine.

XX Human immunodeficiency virus 1.

XX EP570357-A2.

XX 18-NOV-1993.

XX 13-MAY-1993; 93EP-00890100.

XX 14-MAY-1992; 92AT-00000987.

XX 29-AUG-1992; 92US-00932787.

XX (POLI-) POLIMUN SCI IMMUNOLOGISCHE FORSCH GMBH.

XX Katinger H, Rueker F, Himmler G, Muster T, Purtscher M;

PI Malwald G, Steindl F, Trkola A;

XX

DR WPI; 1993-361543/46.
 XX N-PSDB; AAQ51572.
 PT Peptides that induce antibodies which neutralise genetically divergent
 PT HIV-1 isolates - used as recombinant fusion proteins, recombinant
 PT chimeric vaccines or recombinant antibodies.
 PS Claim 1; Page 7; 4lpp; English.
 XX
 CC The sequences given in AAQ51572-96 encode epitopes of gp160 derived from
 CC different strains and isolates of HIV-1. The peptides encoded by these
 CC sequences induce antibodies which neutralise genetically divergent HIV-1
 CC isolates. They bind specifically to the monoclonal antibody 2F5. The
 CC peptides comprise just 6 amino acids derived from the gp160 and represent
 CC highly conserved epitopes which means that antibodies raised against them
 CC will be active against a variety of HIV-1 isolates. The peptides can be
 CC used as recombinant fusion proteins, recombinant chimeric vaccines or as
 CC recombinant antibodies. They may also be used to link the variable
 CC domains of a single chain Fv fragment, or to substitute one or more parts
 CC of a MAb peptide sequence. (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
 CC standardise OS field)
 XX
 XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 2

AA86898
 ID AA86898 standard; peptide; 6 AA.

XX
 AC AA86898;

XX 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 07-SEP-1995 (first entry)

DE Katinger's neutralisation epitope.

KW T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen; gp160; gag;
 KW pol; vaccine; multimeric peptide; AIDS; 3D organisation.

XX Human immunodeficiency virus 1.

XX WO9429339-A1.

XX 22-DEC-1994.

XX 08-JUN-1994; 94WO-CA000317.

XX 09-JUN-1993; 93US-00073378.

XX (CONN-) CONNAUGHT LAB LTD.

XX Sia CDY, Chong P, Klein MH;

XX WPI; 1995-036400/05.

XX Novel tandem synthetic HIV-1 peptide(s) - comprising T-cell epitope of
 PT gag protein linked to B-cell epitope of V3 loop protein of an HIV-1
 PT isolate.

XX Claim 4; Page 16; 69pp; English.

XX This sequence represents a B-cell epitope, which represents the gp41
 CC derived epitope, Katinger's neutralising epitope. This peptide and other

CC peptides containing this sequence may be linked to T-cell epitopes, eg.
 CC T1 or p24E to form a chimeric protein. This chimeric peptide is
 CC recognised by monoclonal antibody 2F5. Chimeric peptides such as this,
 CC may be used in the production of HIV-1 vaccines. These peptide sequences
 CC may also be used in the production of multimeric peptides in which the
 CC peptides are C-terminally modified by the addition of a Lys residue which
 CC is modified on its epsilon amino acid to carry an additional copy of the
 CC peptide molecule. The linear and multimeric peptides may be used for the
 CC treatment of AIDS by acting to displace the binding of HIV virus to human
 CC or animal cells or by disturbing the 3D organisation of the virus.
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to
 CC standardise OS field)

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 3

AA892010

ID AA892010 standard; protein; 6 AA.

XX
 AC AA892010;

XX 16-OCT-2003 (revised)

DT 27-SEP-1996 (first entry)

XX HIV-1 gp41 epitope, for insertion in Mycobacterium alpha antigen.

XX Mycobacterium bovis BCG; AIDS vaccine; surface protein; alpha antigen;

KW Human immunodeficiency virus type 1; fusion protein; gp41 epitope.

XX Human immunodeficiency virus 1.

XX WO9604009-A1.

XX 15-FEB-1996.

XX 31-JUL-1995; 95WO-JP001515.

XX 29-JUL-1994; 94JP-00178462.

XX (AJIN) AJINOMOTO CO INC.

XX (NINA-) JAPAN AGENCY NAT INST HEALTH.

XX Matsuo K, Chujo Y, Yamazaki A, Honda M, Yamazaki S, Taseaka H;

XX WPI; 1996-129127/13.

XX N-PSDB; AAT16054.

XX BCG containing vaccine secretes chimeric protein containing foreign
 PT antigen - has enhanced immunogenicity and antigenicity esp. when used as
 PT an anti-AIDS vaccine.

XX Example 14; Page 29; 56pp; Japanese.

XX Antigenic peptides can be inserted into the alpha-antigen sequence of a
 CC Mycobacterium and secreted from an appropriately transfected M.bovis BCG
 CC cell. The resulting chimeric antigen has greatly enhanced antigenicity
 CC and immunogenicity and is recognised in vivo by B-cells which recognise
 CC the alpha-antigen. The present sequence is that of a HIV-1 gp41 loop
 CC epitope which was incorporated into the alpha antigen. M.bovis BCG cells
 CC secreting a chimeric protein comprising the epitope sequence are useful
 CC as anti-AIDS vaccines. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 6 AA;

Thu Mar 18 10:20:33 2004

us-10-024-329-2.rag

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 4
AAW25868
ID AAW25868 standard; peptide; 6 AA.
XX
AC AAW25868;
XX
DT 25-MAR-2003 (revised)
DT 20-OCT-1997 (first entry)
XX
DE HIV-1 gp41 Katanger's neutralisation epitope.
XX
KW HIV; human immunodeficiency virus; gag; T-cell; B-cell; epitope; env;
KW V3 loop; vaccine; determinant; chimaeric.
XX
OS Synthetic.
XX
FN US5639854-A.
XX
PD 17-JUN-1997.
XX
PF 09-JUN-1994; 94US-00257528.
XX
PR 09-JUN-1993; 93US-00073378.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Klein MH, Sia CDY, Chong P;
XX
DR WPI; 1997-332082/30.
XX
PT Tandem synthetic HIV peptide(s) useful as immunogens - comprising gag
PT protein T-cell epitope linked to env protein B-cell epitope.
XX
PS Example 1; Col 23-24; 41pp; English.
XX
CC The invention relates to new synthetic peptides comprising at least one
CC amino acid sequence comprising an HIV gag protein T-cell epitope linked
CC at its C- or N-terminus to an amino acid sequence comprising a B-cell
CC epitope of the V3 loop of an HIV env protein, which can be used to
CC generate vaccines against HIV-1. The T-cell epitope sequence is pref.
CC selected from the T-helper determinant core peptides P24E, P24N, P24L,
CC P24M and P24H while the B-cell epitopes are derived from HIV strains
CC including CTLB-56, V3MN, CTLB-29, CTLB-55, SF2, LAI, IIB, RP, 26, 2054,
CC 1714 and BX08. The peptides are chimaeric and can be linked to a branched
CC Lys backbone. This is the sequence of the Katanger's neutralisation
CC epitope from the gp41 protein. The peptide is used in the construction of
CC the chimaeric T/B cell epitope peptides AAW25853-67. (Updated on 25-MAR-
CC 2003 to correct PF field.)
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 5
AAW53143
ID AAW53143 standard; peptide; 6 AA.
XX

AAW53143;
XX 20-JUL-1998 (first entry)
XX
DE HIV gp41-contained antibody neutralisation epitope.
XX
KW VJneo; HIV vaccine; codon usage optimisation; HIV; immune response;
KW human immunodeficiency virus; hepatitis; tuberculosis; tumour;
KW env protein; gp140 gene; recombinant.
XX
OS Human immunodeficiency virus.
XX
PN WO9748370-A2.
XX
PD 24-DEC-1997.
XX
PF 17-JUN-1997; 97WO-US010517.
XX
PR 21-JUN-1996; 96US-0020165P.
PR 21-JUN-1996; 96US-0020166P.
PR 16-JUL-1996; 96GB-00014942.
PR 16-JUL-1996; 96GB-00014943.
XX
PA (MERI) MERCK & CO INC.
XX
PI Shiver JW, Davies ME, Freed DC, Liu MA, Perry HC;
XX
DR WPI; 1998-062825/06.
XX
PT DNA encoding protein with codon usage optimised for intended host cell -
PT specifically for DNA vaccines against human immune deficiency virus,
PT allows rev-independent expression of HIV genes.
XX
PS Example 7; Page 39; 113pp; English.
XX
CC This is the gp41-contained antibody neutralisation epitope retained in a
CC HIV gp140 vaccine construct. This is used in a VJneo expression vector
CC for vaccine production containing a new synthetic DNA, encoding a protein
CC or peptide. The synthetic DNA sequence encodes HIV env protein or its
CC fragment and has codons optimised for expression in a non-homologous
CC host. The synthetic DNA sequences are used to increase production of
CC recombinant protein and to induce anti-HIV neutralising antibody, HIV-
CC specific T-cell immune responses or protective immune responses in
CC vertebrates, specifically as HIV vaccines. Optimisation of codons results
CC in increased expression of the DNA in the host. The DNA induces antigen-
CC presenting cells to stimulate cytotoxic and helper T-cells, and effector
CC functions such as lymphokine secretion specific to HIV antigens. Cross-
CC strain protection is achieved without use of adjuvant and the synthetic
CC DNA may provide a longer-lasting response. The env gene includes a high
CC proportion of codons rarely used in mammals, so optimisation will allow
CC this gene to be expressed efficiently in absence of rev. The DNA
CC sequences, more generally, may express antigens from many other
CC pathogens, e.g. hepatitis or tuberculosis, and also from tumours
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 6
AAW67384
ID AAW67384 standard; peptide; 6 AA.
XX
AC AAW67384;
XX
DT 25-JAN-1999 (first entry)
XX

CC T cell epitopes and a sequence encoding 1 or more B cell epitopes and a
 CC carrier. Both the T cell and B cell epitopes are derived from HIV
 CC proteins. The compositions are useful as vaccines against HIV infection.
 CC The composition induces HIV-1-specific polyclonal antibodies that are
 CC opsonising and antiviral. The peptide components may be selected to
 CC induce a response against different viral isolates and in subjects who
 CC recognise different T cell epitopes. (Updated on 17-OCT-2003 to
 CC standardise OS field)

XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 35; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0

QY 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 9
 AAY57748
 ID AAY57748 standard; peptide; 6 AA.
 XX
 AC AAY57748;
 XX 15-MAR-2000 (first entry)
 DT
 DE Peptide amino acid sequence SEQ ID NO:46.
 XX
 KW Recombinant negative strand viral RNA template; virus particle;
 KW RNA directed RNA polymerase complex; expression; chimeric virus; vaccine;
 KW packaging.
 XX Unidentified.
 OS
 XX US6001634-A.
 FN
 PD 14-DEC-1999.
 XX
 XX 29-JUN-1998; 98US-00106377.
 XX
 XX 28-AUG-1989; 89US-00399728.
 PR
 XX 21-NOV-1989; 89US-00440053.
 PR
 XX 22-MAY-1990; 90US-00527237.
 PR
 XX 04-AUG-1992; 92US-00925061.
 PR
 XX 01-FEB-1994; 94US-00190698.
 PR
 XX 01-JUN-1994; 94US-00252508.
 XX
 PA (PALE/) PALESE P.
 PA (GARC/) GARCIA-SASTRE A.
 XX
 XX Palese P, Garcia-Sastre A;
 PI
 XX WPI; 2000-071660/06.
 DR
 XX Chimeric virus containing influenza virus RNA segments, useful for
 XX expressing heterologous gene products in appropriate host cell systems.
 PT
 XX Disclosure; Col 73; 67pp; English.
 PS
 XX The present invention describes a chimeric virus comprising influenza
 CC virus containing a heterologous RNA segment from another strain of
 CC influenza virus or 8 genomic segments from different strains of influenza
 CC virus, with each segment comprising the reverse complement of a mRNA
 CC coding sequence operatively linked to a binding site specific for an RNA-
 CC directed RNA polymerase of a negative strand RNA virus. The recombinant
 CC negative strand virus RNA templates may be used to express heterologous
 CC gene products in appropriate host cell systems and/or to construct
 CC recombinant viruses that express, package and/or present the heterologous
 CC gene product. The expression products and chimeric viruses may be used in
 CC vaccine formulations. AAY57746 to AAY57748, and AAZ56234 to AAZ56290,
 CC represent sequences used in the exemplification of the present invention

XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 35; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0

QY 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 10
 AAB24104
 ID AAB24104 standard; peptide; 6 AA.
 XX
 AC AAB24104;
 XX
 XX 12-SEP-2003 (revised)
 DT
 DT 29-JAN-2001 (first entry)
 XX
 DE HIV-1 gp41 epitope recognised by human MAb 2F5 SEQ ID NO:1.
 XX
 KW HIV-1; human immunodeficiency virus; human; epitope; gp41; MAb;
 KW monoclonal antibody; antiviral; antiHIV; infection; inhibition;
 KW replication.
 XX Human immunodeficiency virus 1.
 OS
 XX WO200055377-A1.
 PN
 XX 21-SEP-2000.
 PD
 XX 15-MAR-2000; 2000WO-US006771.
 PF
 XX 17-MAR-1999; 99US-0124907P.
 PR
 XX 14-MAR-2000; 2000US-00525874.
 PR
 XX (NYBL-) NEW YORK BLOOD CENT INC.
 XX (JIAN/) JIANG S.
 XX (DEBN/) DEBNATH A K.
 PA
 XX Jiang S, Debnath AK;
 FI
 XX WPI; 2000-656011/63.
 DR
 XX Screening assay for antiviral compounds targeted to HIV-1 gp41 core
 XX structure involves utilizing conformation-specific monoclonal antibody,
 XX which is reactive with fusion active gp41 of the virus.
 PT
 XX Example 1c; Page 29; 79pp; English.
 PS
 XX The present invention describes a method for screening (M1) an antiviral
 CC compound (AC) targeted to the HIV-1 gp41 core structure. The method
 CC involves capturing polyclonal antibodies (PAB) directed against trimer of
 CC heterodimer (A) which contains N- and C-peptide (NP,Cp) onto a solid-
 CC phase, to form a PAB-coated solid-phase that is added with mixture of NP,
 CC CP, and AC, adding monoclonal antibody (MAb) directed against (A) and
 CC measuring the binding of MAb. The antivirals identified by the method are
 CC useful for inhibiting HIV-1 replication or infectivity in cells, in
 CC patients and for treating the patients infected with HIV-1. The method
 CC distinguishes the anti-HIV-1 agents targeting the gp41 core domain from
 CC those having different targets. Since the residues located at the
 CC interaction sites in both the N-terminal heptad repeat (NHR) and C-
 CC terminal heptad repeat (CHR) regions of gp41 are highly conserved, the
 CC antiviral agents targeted to the gp41 core are considered to have broader
 CC specificity against infection by HIV strains than those targeted to
 CC gp120. The present sequence represents an HIV-1 gp41 epitope used in an
 CC example from the present invention, which is recognised by the human MAb
 CC 2F5. (Updated on 12-SEP-2003 to standardise OS field)

Sequence 6 AA;
 SQ

Query Match 100.0%; Score 35; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 11

AAG63933
ID AAG63933 standard; peptide; 6 AA.

XX AC AAG63933;

DT 11-SEP-2003 (revised)

DT 29-OCT-2001 (first entry)

XX Amino acid sequence of a HIV-1 gp41 peptide fragment.

XX HIV-1; gp41; viral entry; envelope protein; glycoprotein;
KW viral infection; antiviral.

XX Human immunodeficiency virus 1.

XX WO200159457-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004030.

XX 10-FEB-2000; 2000US-0181543P.

XX 28-SEP-2000; 2000US-0235901P.

XX (PANA-) PANACOS PHARM INC.

XX Wild CT, Allaway GP;

XX WPI; 2001-522493/57.

XX Screening for inhibitors of viral entry structure formation by
PT selectively triggering the formation of one or more critical entry
PT intermediates in cell-surface-expressed viral envelope and probing for
PT its formation.

XX Disclosure; Page 37; 68pp; English.

XX The present sequence represents a fragment of a Human immunodeficiency
CC virus type 1 (HIV-1) gp41 protein. The peptide is used to raise
CC antibodies for use in the method of the invention. The specification
CC describes a method of screening for inhibitors of viral entry structure
CC formation. The method comprises contacting a viral envelope protein or
CC glycoprotein (e.g. gp41) with a triggering agent and a candidate compound
CC to form a mixture, and measuring the effect that the candidate compound
CC has on the formation of conformational intermediates. The effect of the
CC candidate compound can be measured by antibody binding to these
CC conformational intermediates. The compounds identified by the method are
CC useful as inhibitors for inhibiting or preventing viral infection and to
CC treat humans infected with HIV-1 or other viruses. This antiviral
CC compounds can also be used to inactivate viruses in body fluids, e.g.
CC blood or blood compounds used for therapeutic purposes. The assay is also
CC useful for detecting antibodies in virus-infected individuals or virus-
CC infected body fluids or tissues that inhibit entry-relevant
CC conformational changes in one or more viral envelope proteins or
CC glycoproteins. The presence of the antibodies in infected individuals or
CC samples is of prognostic value. (Updated on 11-SEP-2003 to standardise OS
CC field)

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 12

AAB92333
ID AAB92333 standard; peptide; 6 AA.

XX AC AAB92333;

DT 22-JUN-2001 (first entry)

DE Virus related peptide SEQ ID NO:1509.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 699; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention

XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

OS Human immunodeficiency virus 1.
 PN WO200164860-A2.
 XX
 XX
 PD 07-SEP-2001.
 XX
 XX 02-MAR-2001; 2001WO-EP002392.
 PF
 XX 02-MAR-2000; 2000EP-00104338.
 PR
 XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
 PA
 PI Ferko B, Egorov A, Voglauer R;
 XX
 XX WPI; 2001-514840/56.
 DR
 XX Recombinant NS gene of an influenza A virus comprising a functional RNA
 PT binding domain and a gene sequence modification after nucleotide position
 PT 400 of the NS1 gene segment, useful for producing a live attenuated
 PT influenza virus vaccine.
 XX
 PS Claim 3; Page 25; 40pp; English.
 XX
 XX The specification describes a recombinant nonstructural (NS) gene of an
 CC influenza A virus. The gene comprises a functional RNA binding domain and
 CC a gene sequence modification after nucleotide position 400 of the NS1
 CC gene segment, counted on the basis of influenza A/PR/8/34 virus, where
 CC the modification bars transcription of the remaining portion of the NS1
 CC gene segment. The recombinant NS gene is used to produce a vaccine, which
 CC is useful for prophylactic or therapeutic application against a viral
 CC infection, preferably against influenza or HIV-1 infection. Influenza
 CC virus transfectants that contain the modified NS gene may have an
 CC interferon (IFN) inducing phenotype, but may or may not be sensitive
 CC towards IFN. The present sequence represents a gp41 epitope, and was
 CC used to modify the NS genes of the invention. (Updated on 11-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6
 RESULT 16
 ABB07403
 ID ABB07403 standard; peptide; 6 AA.
 XX
 AC ABB07403;
 XX
 DT 29-AUG-2003 (revised)
 DT 09-APR-2002 (first entry)
 XX
 XX HIV-1 gp41 epitope fragment.
 DE
 XX Coat protein; potyvirus; bean yellow mosaic virus; BYMV; immunogenic;
 KW plant virion; vaccine; NDV; Newcastle Disease virus; HIV; gp41; PVX; PVY;
 KW potato virus; epitope.
 KW
 XX Human immunodeficiency virus 1.
 OS
 XX WO200200169-A2.
 PN
 XX 03-JAN-2002.
 XX
 XX 26-JUN-2001; 2001WO-US020272.
 PF
 XX 26-JUN-2000; 2000US-00603997.
 PR
 XX (UYQI) UNIV QINGHUA.
 PA (JIAN-) JIANGXI DRAGON FLY SCI & TECHNOLOGY CO LT.
 PA (BEIJ-) BEIJING GUOXIWEIYE HIGH TECHNOLOGY DEV C.

PA (USDA) US DEPT OF AGRICULTURE.
 XX
 XX Hammond R, Zhao Y, Hammond J;
 XX
 DR WPI; 2002-139854/18.
 XX
 XX New cDNA constructs comprising a bean yellow mosaic virus (BYMV) DNA
 PT sequence or a DNA sequence encoding a fusion coat protein, useful for
 PT generating quantities of immunogenic peptides for vaccine and antibody
 PT production.
 XX
 XX Claim 5; Page 26; 52pp; English.
 PS
 XX The invention provides a cDNA construct, containing a DNA sequence that
 CC encodes a fusion coat protein comprising a truncated potyvirus coat
 CC protein and a foreign antigenic peptide. The cDNA construct comprises a
 CC bean yellow mosaic virus (BYMV) DNA. The cDNA constructs and vectors are
 CC useful for generating the expressed immunogenic peptides. The cDNA
 CC constructs and vectors are useful for systemically infecting a plant to
 CC produce stable recombinant plant virions expressing foreign peptides, as
 CC a means of producing and purifying large amounts of foreign peptides to
 CC be used as genetically engineered vaccines or for antibody production.
 CC These are particularly useful for producing and purifying large amounts
 CC of NDV (newcastle disease virus) vaccine. A method of producing a foreign
 CC antigenic peptide in a plant comprises infecting a host plant with PVY
 CC (potato virus Y) virions, inoculating the PVY-infected host plant with
 CC the infectious RNA, culturing the plant under conditions to foster plant
 CC growth and transencapsidation; and recovering the transencapsidated PVY
 CC virions from the leaves of the plant. The PVY virions contain foreign of
 CC antigenic peptide inserts on the exposed surface of the coat protein of
 CC the virion, the inserts resulting from a transencapsidation process
 CC during virion assembly where copies of PVX (potato virus X) coat protein
 CC containing the fusion coat protein and copies of PVY coat protein
 CC assemble to form the PVY capsid. The present sequence represents HIV-1
 CC gp41 epitope fragment. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6
 RESULT 17
 AAO14868
 ID AAO14868 standard; peptide; 6 AA.
 XX
 AC AAO14868;
 XX
 DT 19-JUL-2002 (first entry)
 DT
 DS HIV epitope peptide 2.
 XX
 KW HIV; acquired immunodeficiency syndrome; AIDS; vaccine;
 KW HIV neutralising epitope; CTL epitope.
 XX
 OS Human immunodeficiency virus.
 XX
 XX WO200226253-A1.
 PN
 XX 04-APR-2002.
 PD
 XX 20-JUL-2001; 2001WO-CN001190.
 XX
 PF 18-AUG-2000; 2000CN-00123487.
 XX
 PR (UYQI) UNIV QINGHUA.
 PA (JIAN-) JIANGXI DRAGON FLY SCI & TECHNOLOGY CO LT.
 PA (BEIJ-) BEIJING GUOXIWEIYE HIGH TECHNOLOGY DEV C.

[illegible]

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 20
ADC79307
ID ADC79307 standard; peptide; 6 AA.
XX
AC ADC79307;
DT 01-JAN-2004 (first entry)
XX
DE HIV-1 gp41 peptide SEQ ID NO:2.
XX
KW immune response; anti-HIV; vaccine; HIV infection.
KW Human immunodeficiency virus 1.
OS
XX
PN WO2003075849-A2.
XX
PD 18-SEP-2003.
XX
PF 06-MAR-2003; 2003WO-US007073.
XX
PR 06-MAR-2002; 2002US-0362247P.
XX
PA (UYAR-) UNIV ARIZONA.
XX
PI Mor TS, Matoba N, Arntzen CJ;
XX
DR WPI; 2003-779033/73.
XX
PT New composition comprising a peptide and a cholera toxin, useful for
PT enhancing immune response in an animal against HIV infection.
XX
PS Claim 1; SEQ ID NO 2; 33pp; English.

XX The present invention describes a composition (C) for enhancing the
CC immune response in an animal. (C) comprises a peptide selected from the
CC group ADC79306, ADC79307, ADC79308, ADC79309, ADC79310, ADC79311 and
CC ADC79312. Also described: (1) enhancing the immune response in an animal;
CC (2) delivering a cargo protein to an animal cell; (3) genetically-
CC modified living cell capable of enhancing immune response in an animal
CC comprising a first DNA sequence encoding a peptide; and (4) constructing
CC a fusion protein for enhancing immune response in an animal. (C) has anti-
CC -HIV activities; and can be used in vaccines. The composition (C) can be
CC used for enhancing the immune response in an animal against HIV
CC infection.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 21
AAR71631
ID AAR71631 standard; peptide; 7 AA.
XX
AC AAR71631;
XX
DT 25-MAR-2003 (revised)
DT 20-SEP-1995 (first entry)
XX
DE HIV-1 gp41 peptide.
XX
KW HIV-1; gp41; gp160; 2F5 epitope; antibody; cell fusion; AIDS; vaccine;

Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 22
AAR94444
ID AAR94444 standard; peptide; 7 AA.
XX
AC AAR94444;
XX
DT 16-OCT-2003 (revised)
DT 31-MAY-1996 (first entry)
XX
DE HIV-1 gp41 B-cell and neutralising epitope.
XX
KW Molecular presentation; FHV; virion-like particle; capsid protein;
KW capsomer; RNA-2 gene; epitope; HIV-1; vaccine.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9605293-A1.
XX
PD 22-FEB-1996.
XX
PF 04-AUG-1995; 95WO-EP003114.
XX
PR 08-AUG-1994; 94AT-00001545.
XX
PA (UNNA-) UNITED NATIONS IND DEV ORG.
XX
PI Baralle FE, Scodeller E, Tisminetzky S;
XX
DR WPI; 1996-139691/14.
XX
PT New molecular presentation system - comprising a viral protein from a

immunogen; therapy; human immunodeficiency virus type 1;
monoclonal antibody; MAB.
Synthetic.
WO9507354-A1.
16-MAR-1995.
12-SEP-1994; 94WO-EP003039.
11-SEP-1993; 93EP-00114631.
(POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
Katinger H, Muster T;
WPI; 1995-123428/16.
New peptide(s) corresponding to a HIV-1 gp 160 epitope - used to elicit
antibodies which neutralise different HIV-1 strains and inhibit cell
fusion caused by HIV-1.
Claim 1; Page 17; 28pp; English.
The peptides given in AAR71631-36 are based on amino acids 661-668 of HIV
-1 isolate BH10 gp41, the epitope of human MAB 2F5. The peptides may be
inserted into antigenic sites of a viral protein, e.g. influenza virus
hemagglutinin, by gene fusion, for HIV-1 vaccine development. (Updated on
25-MAR-2003 to correct PN field.)
Sequence 7 AA;

Thu Mar 18 10:20:33 2004

us-10-024-329-2.rag

```

PT small insect virus in which heterologous amino acid sequences are
PT inserted.
XX Disclosure; Page 7; 39pp; English.
XX
XX An HIV-1 gp41 B-cell and neutralising epitope (AAR94444) may be inserted
CC into the outward-directed L1, L2, L3, L4 or L5 loop of the Flock House
CC virus capsid protein (AAR88755). The capsid protein provides a
CC conformationally suitable location for this (or other, see AAR94430-43
CC and AAR94445) heterologous peptides. A molecular presentation system is
CC obtd. The FHV recombinant capsomer can be expressed in E. coli.
CC Alternatively, expression in insect cells using a baculovirus vector
CC results in prodn. of mature virus-like particles. (Updated on 16-OCT-2003
CC to standardise OS field)
XX
XX Sequence 7 AA;
SQ
Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 1 ELDKWA 6
RESULT 23
AAW25897
ID AAW25897 standard; peptide; 7 AA.
XX
XX AAW25897;
XX
XX 25-MAR-2003 (revised)
DT 22-OCT-1997 (first entry)
XX
XX Peptide containing Katinger's neutralisation epitope.
DE
XX HIV; human immunodeficiency virus; gag; T-cell; B-cell; epitope; env;
KW V3 loop; vaccine; determinant; chimaeric.
KW
XX Synthetic.
OS
XX US5639854-A.
PN
XX 17-JUN-1997.
PD
XX 09-JUN-1994; 94US-00257528.
PF
XX 09-JUN-1993; 93US-00073378.
PR
XX (CONN-) CONNAUGHT LAB LTD.
XX
XX Klein MH, Sia CDY, Chong P;
PI
XX WPI; 1997-332082/30.
DR
XX Tandem synthetic HIV peptide(s) useful as immunogens - comprising gag
PT protein T-cell epitope linked to env protein B-cell epitope.
PT
XX Disclosure; Col 71; 41pp; English.
PS
XX The invention relates to new synthetic peptides comprising at least one
CC amino acid sequence comprising an HIV gag protein T-cell epitope linked
CC at its C- or N-terminus to an amino acid sequence comprising a B-cell
CC epitope of the V3 loop of an HIV env protein, which can be used to
CC generate vaccines against HIV-1. The T-cell epitope sequence is pref.
CC selected from the T-helper determinant core peptides P24E, P24N, P24L,
CC P24M and P24H while the B-cell epitopes are derived from HIV strains
CC including CTIB-56, V3MN, CTIB-29, CTIB-55, SF2, LAI, IIB, RF, 26, 2054,
CC 1714 and BX08. The peptides are chimaeric and can be linked to a branched
CC Lys backbone. This sequence represents peptide containing the sequence of
CC the Katinger's neutralisation peptide (AAW25868). The peptide is used in
CC the construction of the chimaeric T-helper determinant epitopes AAW25893-
CC

```

```

CC 96. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 1 ELDKWA 6
RESULT 24
AAW67413
ID AAW67413 standard; peptide; 7 AA.
XX
XX AAW67413;
XX
XX 25-JAN-1999 (first entry)
DT
XX HIV-1 gp41 protein neutralisation epitope.
DE
XX Immunogen; vaccine; HIV-1; T-cell; B-cell; epitope; core protein; gp120;
KW V3 loop.
KW
XX Synthetic.
OS
XX Human immunodeficiency virus 1.
PN
XX US5817754-A.
PD
XX 06-OCT-1998.
PF
XX 05-JUN-1995; 95US-00464329.
PR
XX 09-JUN-1993; 93US-00073378.
PR
XX 09-JUN-1994; 94US-00257528.
XX
XX (CONN-) CONNAUGHT LAB LTD.
XX
XX Chong P, Klein MH, Sia CDY;
PI
XX WPI; 1998-556461/47.
XX
XX Synthetic human immunodeficiency virus-1 peptide(s) - containing T-cell
PT epitope and B-cell epitope(s) are candidate vaccines against HIV-1.
XX
XX Disclosure; Col 9; 40pp; English.
PS
XX The invention relates to a novel immunogenic composition for use in
CC vaccines for the treatment of HIV-1 comprising an HIV-1-derived T-cell
CC epitope linked to an HIV-1-derived B-cell epitope. The T-cell epitopes
CC are generally designed based on the p24 core protein and the B-cell
CC epitopes from the V3 loop of the gp120 protein from various HIV-1
CC strains. This sequence corresponds to the neutralisation epitope from the
CC HIV-1 protein gp41
XX
XX Sequence 7 AA;
Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 1 ELDKWA 6
RESULT 25
AAW99911
ID AAW99911 standard; peptide; 7 AA.
XX
XX AAW99911;

```


PT Three dimensional structure of Fab' fragment of human immunodeficiency
PT virus-1 cross-neutralizing monoclonal antibody 2F5, complexed or
PT uncomplexed with a peptide for construction of peptide analogs and
PT peptide mimetics.

XX Claim 13; Page 30; 42pp; English.

XX The invention relates to an isolated crystal of the Fab' fragment of
CC monoclonal antibody (Mab) 2F5. Mab 2F5 binds an epitope (AAB29401) of the
CC HIV-1 envelope protein gp41. The Mab 2F5 Fab' fragment may be complexed
CC or uncomplexed with the gp41 epitope (or a functional analogue thereof) in
CC the crystal of the invention. Elucidation of the three- dimensional
CC structures of 2F5 Fab' in the epitope-complexed and uncomplexed states
CC enables construction of peptide mimetics constrained in the same beta-
CC turn-like configuration as seen in the crystal structure of the complex,
CC providing an increased immunogenicity to the epitope sequence.

CC Elucidation of the crystal structure of Fab' 2F5 when bound to the
CC peptide GluLeuAspLysTrpSer provides details of the actual conformation of
CC the peptide epitope when it is bound to the antibody. The conformation of
CC the peptide epitope provides the basis for the provision of peptide
CC analogs, peptide mimetics and other antigens which are useful as
CC components of an anti-HIV vaccine. The present sequence represents the
CC HIV-1 gp41 epitope which binds to Mab 2F5. (Updated on 12-SEP-2003 to
CC standardise OS field)

XX Sequence 7 AA;

Query Match 100.0%; Score 35; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 28
AAU70190
ID AAU70190 standard; peptide; 7 AA.
AC AAU70190;
XX 14-FEB-2002 (first entry)
XX P3 peptide linear binding region.
XX Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;
KW anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
KW alpha-helical region; ectodomain.
XX Homo sapiens.
XX WO200170262-A2.
XX 27-SEP-2001.
XX 15-MAR-2001; 2001WO-US008108.
XX 17-MAR-2000; 2000US-0189981P.
XX (PANA-) PANACOS PHARM INC.
XX Wild CT, Allaway GP;
XX WPI; 2001-626098/72.
XX Immunogenic composition for inhibiting HIV infection, comprises viral
PT envelope protein or its fragment exterior to viral membrane, a
PT stabilising peptide, and, optionally, viral cell surface receptor or its
PT fragment.
XX Example 12; Page 65; 84pp; English.

CC The invention relates to methods of generating immunogens that elicit
CC neutralising antibodies which target regions of viral envelope proteins
CC such as the gp120/gp41 glycoprotein 120(glycoprotein 41) complex of HIV-
CC 1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and
CC AAU70677-AAU70743 represent stabilising peptides modelling the alpha-
CC helical regions of the ectodomain of the HIV-1 transmembrane protein to
CC stabilise fusion-active intermediate structures, which can be used as
CC vaccine immunogens. Immunogenic compositions comprise a viral envelope
CC protein or its fragment exterior to the viral membrane, a stabilising
CC peptide to disrupt formation of structural intermediates necessary for
CC viral fusion and entry, and optionally, a viral cell surface receptor or
CC its fragment. The stabilising peptide is capable of associating with the
CC envelope protein or its fragment to form a stabilised, fusion active
CC structure. Antibody binding assays are used to determine the ability of
CC immunogen vaccines to generate an immune response to various forms of
CC envelope. Virus neutralisation assays can be used to characterise the
CC antibody response raised against HIV-1 gp41 domains. The sequences and
CC methods are useful for inhibiting HIV infection, for inducing an immune
CC response in an animal and for raising antibodies

XX Sequence 7 AA;

Query Match 100.0%; Score 35; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 29
AAG63975
ID AAG63975 standard; peptide; 7 AA.
XX AAG63975;
XX 11-SEP-2003 (revised)
DT 13-NOV-2001 (first entry)
XX Amino acid sequence of a HIV-1 gp41 derived peptide.
DE Nonstructural gene; NS gene; influenza A virus; NS1 gene; vaccine;
KW viral infection; influenza infection; HIV-1 infection; gp41.
XX Human immunodeficiency virus 1.
XX WO200164860-A2.
XX 07-SEP-2001.
XX 02-MAR-2001; 2001WO-EP002392.
XX 02-MAR-2000; 2000EP-00104338.
XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX Ferko B, Egorov A, Voglauer R;
XX WPI; 2001-514840/56.
XX Recombinant NS gene of an influenza A virus comprising a functional RNA
PT binding domain and a gene sequence modification after nucleotide position
PT 400 of the NS1 gene segment, useful for producing a live attenuated
PT influenza virus vaccine.
XX Claim 3; Page 25; 40pp; English.
XX The specification describes a recombinant nonstructural (NS) gene of an
CC influenza A virus. The gene comprises a functional RNA binding domain and
CC a gene sequence modification after nucleotide position 400 of the NS1
CC gene segment counted on the basis of influenza A/PR/8/34 virus, where
CC the modification bars transcription of the remaining portion of the NS1


```
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 35; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 32
AAU97480
ID AAU97480 standard; peptide; 7 AA.
AC AAU97480;
XX
DT 29-AUG-2003 (revised)
DT 13-AUG-2002 (first entry)
XX
DE HIV-1 infection inhibitory activity associated peptide #3.
XX
KW Human immunodeficiency virus; HIV; antisense peptide; gp41; T20;
KW infection inhibitory activity; envelope glycoprotein; gp160;
KW infection inhibition; HIV-1_1_1B; infection mechanism; virucide;
KW anti-HIV; HIV-antagonist.
XX
OS Human immunodeficiency virus 1.
XX
PN JP2002080999-A.
XX
PD 27-MAR-2002.
XX
PF 13-SEP-2000; 2000JP-00277747.
PR 13-SEP-2000; 2000JP-00277747.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2002-430873/46.
XX
PT Antisense peptides with HIV-1 infection inhibitory activity having gp41
PT amino acid sequence in T20 of HIV-1 envelope glycoprotein gp160 molecules
PT useful for investigation of infection mechanism of HIV-1.
XX
PS Example B; Page 9; 16pp; Japanese.
XX
CC The present invention relates to new antisense peptides with HIV-1
CC infection inhibitory activity having gp41 amino acid sequence in T20 of
CC HIV-1 envelope glycoprotein gp160 molecules. The peptides of the
CC invention are useful for infection inhibition of HIV-1_1_1B. The
CC invention is advantageous as it can be used for treatment of HIV-1 and
CC investigation of its infection mechanism. The present amino acid sequence
CC represents one of a collection (AAU97478-AAU97487) of human
CC immunodeficiency virus (HIV-1) infection inhibitory activity associated
CC peptides. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 35; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 33
ABR39671
ID ABR39671 standard; peptide; 7 AA.
XX
```

```
AC ABR39671;
XX
DT 23-OCT-2003 (revised)
DT 23-JUN-2003 (first entry)
XX
DE HIV-1 gp41 peptide fragment.
XX
KW HIV-1; immune response; gp41; anti-HIV; vaccine; mAb 4E10-IgG1;
KW anti-idiotypic antibody.
XX
OS Human immunodeficiency virus 1.
XX
PN WO2003022879-A2.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-EP010070.
XX
PR 07-SEP-2001; 2001US-0318091P.
XX
PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX
PI Stiegler G, Kunert R, Katinger H;
XX
DR WPI; 2003-354526/33.
XX
PT New peptide that interferes with HIV-1 entry into target cells and
PT preferably induces an HIV-1 neutralizing immune response, where the
PT peptide is a fragment of gp41 of HIV-1, useful for inhibiting or
PT preventing HIV-1 infection.
XX
PS Example 7; Page 20; 33pp; English.
XX
CC The invention relates to a peptide that interferes with HIV-1 entry into
CC target cells and preferably induces an HIV-1 neutralizing immune
CC response, where the peptide is a fragment of gp41 of HIV-1. The peptide,
CC antibody, composition and vaccine are useful for inhibiting or preventing
CC HIV-1 infection. The mAb 4E10-IgG1 is useful for eliciting or screening
CC for an anti-idiotypic antibody that is reactive with the 4E10 binding
CC paratope of mAb 4E10-IgG1, and that preferably mimics a fragment of gp41
CC of HIV. Sequences ABR39667-675 represent HIV-1 gp41 peptide fragments.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 7 AA;
Query Match 100.0%; Score 35; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 34
ABR62950
ID ABR62950 standard; peptide; 7 AA.
XX
AC ABR62950;
XX
DT 04-DEC-2003 (first entry)
XX
DE HIV-1 virus envelope ectodomain gp41 core epitope variant.
XX
KW HIV-1; anti-idiotypic; antibody; anti-HIV; virucide; vaccine.
XX
OS Synthetic.
XX
PN WO2003059953-A2.
XX
PD 24-JUL-2003.
XX
PF 17-JAN-2003; 2003WO-EP0000455.
```

```

XX PR 17-JAN-2002; 2002EP-00001250.
XX PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX PI Kunert R, Weik R, Stiegler G, Katinger H;
XX DR WPI; 2003-598509/56.
XX FS Claim 2; Page 15; 32pp; English.
XX CC The present sequence is that of a variant of a highly conserved epitope
XX CC sequence (see ABR62944) on the HIV-1 envelope ectodomain gp41. The
XX CC invention provides an antibody, or its fragment, which is reactive with
XX CC HIV-1 neutralising antibody 2F5 (ECACC 90091704) and which inhibits or
XX CC prevents the HIV-1 neutralisation activity of 2F5 and/or the binding of
XX CC 2F5 to HIV-1 gp41. The antibody preferably inhibits or prevents the
XX CC binding of 2F5 to proteins or peptides that comprise the HIV-1 gp41
XX CC conserved epitope or its variants (see ABR62945-55). Upon administration
XX CC to a mammal, the antibody elicits Ab3-type antibodies that have HIV-1
XX CC neutralising activity and/or that compete with 2F5 for binding to
XX CC proteins comprising the conserved epitope or its variants. The antibody
XX CC is preferably an Ab2-type antibody which is anti-idiotypic to 2F5, is
XX CC monoclonal and is produced by hybridoma cell line 3G6 (ECACC 01100279),
XX CC or is a chimeric or humanized antibody. The antibody or its fragment may
XX CC be coupled, linked or fused to an immunoreactive molecule, such as
XX CC interleukin-4 or interleukin-15, that increases or intensifies a B cell
XX CC response. It can be used as a screening tool, diagnostic or therapeutic
XX CC agent, or as a vaccine against HIV-1 infection.
XX SQ Sequence 7 AA;
XX Query Match 100.0%; Score 35; DB 7; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1 ELDKWA 6
XX Db 1 ELDKWA 6
XX RESULT 35
XX ID ABR62947 standard; peptide; 7 AA.
XX AC ABR62947;
XX XX 04-DEC-2003 (first entry)
XX DT HIV-1 virus envelope ectodomain gp41 core epitope variant.
XX DE HIV-1; anti-idiotypic; antibody; anti-HIV; virucide; vaccine.
XX KW HIV-1; anti-idiotypic; antibody; anti-HIV; virucide; vaccine.
XX OS Synthetic.
XX XX WO2003059953-A2.
XX PN 24-JUL-2003.
XX PD 17-JAN-2003; 2003WO-EP000455.
XX PF 17-JAN-2002; 2002EP-00001250.
XX PR (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX PA Kunert R, Weik R, Stiegler G, Katinger H;
XX PI WPI; 2003-598509/56.
XX DR
XX FS Claim 2; Page 15; 32pp; English.
XX CC The present sequence is that of a variant of a highly conserved epitope
XX CC sequence (see ABR62944) on the HIV-1 envelope ectodomain gp41. The
XX CC invention provides an antibody, or its fragment, which is reactive with
XX CC HIV-1 neutralising antibody 2F5 (ECACC 90091704) and which inhibits or
XX CC prevents the HIV-1 neutralisation activity of 2F5 and/or the binding of
XX CC 2F5 to HIV-1 gp41. The antibody preferably inhibits or prevents the
XX CC binding of 2F5 to proteins or peptides that comprise the HIV-1 gp41
XX CC conserved epitope or its variants (see ABR62945-55). Upon administration
XX CC to a mammal, the antibody elicits Ab3-type antibodies that have HIV-1
XX CC neutralising activity and/or that compete with 2F5 for binding to
XX CC proteins comprising the conserved epitope or its variants. The antibody
XX CC is preferably an Ab2-type antibody which is anti-idiotypic to 2F5, is
XX CC monoclonal and is produced by hybridoma cell line 3G6 (ECACC 01100279),
XX CC or is a chimeric or humanized antibody. The antibody or its fragment may
XX CC be coupled, linked or fused to an immunoreactive molecule, such as
XX CC interleukin-4 or interleukin-15, that increases or intensifies a B cell
XX CC response. It can be used as a screening tool, diagnostic or therapeutic
XX CC agent, or as a vaccine against HIV-1 infection.
XX SQ Sequence 7 AA;
XX Query Match 100.0%; Score 35; DB 7; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1 ELDKWA 6
XX Db 1 ELDKWA 6
XX RESULT 36
XX ID AAR71632 standard; peptide; 8 AA.
XX AC AAR71632;
XX XX 25-MAR-2003 (revised)
XX DT 20-SEP-1995 (first entry)
XX XX HIV-1 gp41 peptide.
XX DE HIV-1; gp41; gp160; 2F5 epitope; antibody; cell fusion; AIDS; vaccine;
XX KW immunogen; therapy; human immunodeficiency virus type 1;
XX KW monoclonal antibody; Mab.
XX OS Synthetic.
XX XX WO9507354-A1.
XX PN 16-MAR-1995.
XX PD 12-SEP-1994; 94WO-EP003039.
XX PF 11-SEP-1993; 93EP-00114631.
XX PR (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX PA Katinger H, Muster T;
XX PI WPI; 1995-123428/16.
XX DR
XX XX New peptide(s) corresponding to a HIV-1 gp 160 epitope - used to elicit
XX PT antibodies which neutralise different HIV-1 strains and inhibit cell
XX FT fusion caused by HIV-1.
XX XX

```

PS Claim 1; Page 17; 28pp; English.

XX The peptides given in AAR71631-36 are based on amino acids 661-668 of HIV

CC -1 isolate BR10 gp41, the epitope of human Mab 2F5. The peptides may be

CC inserted into antigenic sites of a viral protein, e.g. influenza virus

CC hemagglutinin, by gene fusion, for HIV-1 vaccine development. (Updated on

CC 25-MAR-2003 to correct PN field.)

XX Sequence 8 AA;

SQ

Query Match 100.0%; Score 35; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. NO. 1.4e+06; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0;

Qy 1 ELDKWA 6

Db 2 ELDKWA 7

RESULT 37

AAV05254

ID AAY05254 standard; peptide; 8 AA.

XX

AC AAY05254;

XX

DT 17-OCT-2003 (revised)

DT 21-JUN-1999 (first entry)

DE MN-HIV gp41 fragment.

XX HIV; gp41; viral load reduction; viral titre reduction; HIV infection;

KW immunogenic carrier; vaccine; therapy.

KW

OS Human immunodeficiency virus 1.

XX

XX WO9917789-A1.

XX

PD 15-APR-1999.

XX

PF 06-OCT-1998; 98WO-US020966.

XX

PR 07-OCT-1997; 97US-00946525.

XX

PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.

XX

PI Rubinstein A, Bloom BR, Devash Y, Cryz SJ;

XX

DR WPI; 1999-263900/22.

XX

FT Reducing load of human immune deficiency virus.

XX

PS Claim 3; Page 11; 144pp; English.

XX

CC This sequence represents a fragment from the gp41 protein of the MN

CC strain of HIV. The invention relates to a method for reducing the level

CC of HIV (human immune deficiency virus) titre in a mammal, by

CC administering a composition (A) containing at least one peptide (such as

CC this sequence) coupled to an immunogenic carrier. (A) are used to treat

CC or prevent HIV infections, including prevention of maternal-fetal

CC transfer. (A) induces a long-term neutralising antibody response in the

CC serum; high levels of mucosal antibodies and cytotoxic T cells, and thus

CC reduces viral load and prevents or inhibits progression of disease.

CC (Updated on 17-OCT-2003 to standardise OS field)

XX

SQ

Query Match 100.0%; Score 35; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. NO. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6

Db 3 ELDKWA 8

RESULT 38

ABP12065

ID ABP12065 standard; peptide; 8 AA.

XX

AC ABP12065;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX HIV A02 super motif env peptide #122.

DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

XX WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Cellis E, Kubo RT, Grey HW;

XX

DR WPI; 2001-354887/37.

XX

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 116; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present

CC in whole antigens can be avoided with the use of group-based vaccines. An

CC additional advantage of an group-based vaccine approach is the ability to

CC combine selected groups (CTL and HTL), and further, to modify the

CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP1501 to ABP25412

CC represent peptide sequences used in the exemplification of the present

CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ

Query Match 100.0%; Score 35; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. NO. 1.4e+06; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0;

Qy 1 ELDKWA 6

Db 1 ELDKWA 6


```

RESULT 39
ABP12063
ID ABP12063 standard; peptide; 8 AA.
XX
XX
AC ABP12063;
XX
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
XX
DE HIV A02 super motif env peptide #120.
XX
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
XX
OS Human immunodeficiency virus 1.
XX
XX
PN WO200124810-A1.
XX
XX
PD 12-APR-2001.
XX
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
XX
PR 05-OCT-1999; 99US-00412863.
XX
XX
PA (EPIM-) EPIMUNE INC.
XX
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX
DR WPI; 2001-354887/37.
XX
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
XX
PS Claim 32; Page 116; 448pp; English.
XX
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 35; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 3 ELDKWA 8

RESULT 40
ABP15180
ID ABP15180 standard; peptide; 8 AA.
XX
XX
AC ABP15180;
XX
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
XX
DE HIV A24 super motif env peptide #60.
XX
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
XX
OS Human immunodeficiency virus 1.
XX
XX
PN WO200124810-A1.
XX
XX
PD 12-APR-2001.
XX
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
XX
PR 05-OCT-1999; 99US-00412863.
XX
XX
PA (EPIM-) EPIMUNE INC.
XX
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX
DR WPI; 2001-354887/37.
XX
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
XX
PS Claim 32; Page 180; 448pp; English.
XX
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 35; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 41
ABP20177
ID ABP20177 standard; peptide; 8 AA.
XX
XX

```

AC ABP20177;
XX 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
XX HIV A03 motif env peptide #381.
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus 1.
OS
XX WO200124810-A1.
PN
XX
XX 12-APR-2001.
PD
XX 05-OCT-2000; 2000WO-US027766.
PF
XX 05-OCT-1999; 99US-00412863.
PR
XX (EPTM-) EPIMMUNE INC.
PA
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
PI
XX WPI; 2001-354887/37.
DR
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
PT
XX Claim 32; Page 283; 448pp; English.
PS
XX The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 35; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 3 ELDKWA 8
RESULT 42
AAU97481
ID AAU97481 standard; peptide; 8 AA.
XX
XX AAU97481;
AC
XX

DT 29-AUG-2003 (revised)
DT 13-AUG-2002 (first entry)
XX
XX HIV-1 infection inhibitory activity associated peptide #4.
XX Human immunodeficiency virus; HIV; antisense peptide; gp41; T20;
KW infection inhibitory activity; envelope glycoprotein; gp160;
KW infection inhibition; HIV-1_1_1B; infection mechanism; virucide;
KW anti-HIV; HIV-antagonist.
XX
XX Human immunodeficiency virus 1.
OS
XX JP2002088099-A.
PN
XX 27-MAR-2002.
PD
XX 13-SEP-2000; 2000JP-00277747.
PF
XX 13-SEP-2000; 2000JP-00277747.
PR
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA
XX WPI; 2002-430873/46.
DR
XX Antisense peptides with HIV-1 infection inhibitory activity having gp41
PT amino acid sequence in T20 of HIV-1 envelope glycoprotein gp160 molecules
PT useful for investigation of infection mechanism of HIV-1.
PT
XX Example B; Page 9; 16pp; Japanese.
PS
XX The present invention relates to new antisense peptides with HIV-1
CC infection inhibitory activity having gp41 amino acid sequence in T20 of
CC HIV-1 envelope glycoprotein gp160 molecules. The peptides of the
CC invention are useful for infection inhibition of HIV-1_1_1B. The
CC invention is advantageous as it can be used for treatment of HIV-1 and
CC investigation of its infection mechanism. The present amino acid sequence
CC represents one of a collection (AAU97478-AAU97487) of human
CC immunodeficiency virus (HIV-1) infection inhibitory activity associated
CC peptides. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 35; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 2 ELDKWA 7
RESULT 43
ABR62953
ID ABR62953 standard; peptide; 8 AA.
XX
XX ABR62953;
AC
XX
XX 04-DEC-2003 (first entry)
DT
XX HIV-1 virus envelope ectodomain gp41 core epitope variant.
DE
XX HIV-1; anti-idiotypic; antibody; anti-HIV; virucide; vaccine.
KW
XX Synthetic.
OS
XX WO2003059953-A2.
PN
XX 24-JUL-2003.
PD
XX 17-JAN-2003; 2003WO-EP0000455.
PF
XX 17-JAN-2002; 2002EP-00001250.
PR
XX
XX

PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

PI Kunert R, Weik R, Stiegler G, Katinger H;

XX WPI; 2003-598509/56.

XX New anti-idiotypic antibody inducing HIV-1 neutralizing antibodies,
PT useful as a screening tool or diagnostic agent, and for the manufacture
PT of a vaccine, for prophylactic or therapeutic application against HIV-1
PT infection.

XX Claim 2; Page 15; 32pp; English.

XX The present sequence is that of a variant of a highly conserved epitope
CC sequence (see ABR62944) on the HIV-1 envelope ectodomain gp41. The
CC invention provides an antibody, or its fragment, which is reactive with
CC HIV-1 neutralising antibody 2F5 (ECACC 90091704) and which inhibits or
CC prevents the HIV-1 neutralisation activity of 2F5 and/or the binding of
CC 2F5 to HIV-1 gp41. The antibody preferably inhibits or prevents the
CC binding of 2F5 to proteins or peptides that comprise the HIV-1 gp41
CC conserved epitope or its variants (see ABR62945-55). Upon administration
CC to a mammal, the antibody elicits Ab3-type antibodies that have HIV-1
CC neutralising activity and/or that compete with 2F5 for binding to
CC proteins comprising the conserved epitope or its variants. The antibody
CC is preferably an Ab2-type antibody which is anti-idiotypic to 2F5, is
CC monoclonal and is produced by hybridoma cell line 3G6 (ECACC 01100279),
CC or is a chimeric or humanized antibody. The antibody or its fragment may
CC be coupled, linked or fused to an immunoreactive molecule, such as
CC interleukin-4 or interleukin-15, that increases or intensifies a B cell
CC response. It can be used as a screening tool, diagnostic or therapeutic
CC agent, or as a vaccine against HIV-1 infection

XX Sequence 8 AA;

Query Match 100.0%; Score 35; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Qy 1 ELDKWA 6
|||||
Db 2 ELDKWA 7

RESULT 44

AAR71637
ID AAR71637 standard; peptide; 9 AA.

XX AC AAR71637;

XX DT 25-MAR-2003 (revised)

XX DT 20-SEP-1995 (first entry)

XX DE Immunization control peptide.

XX HIV-1; gp41; gp160; 2F5 epitope; antibody; cell fusion; AIDS; vaccine;
KW immunogen; therapy; human immunodeficiency virus type 1;
KW monoclonal antibody; Mab; hemagglutinin; baculovirus; Sf9;
KW Spodoptera frugiperda.

XX Synthetic.

XX WO9507354-A1.

XX PD 16-MAR-1995.

XX PF 12-SEP-1994; 94WO-EP0030339.

XX PR 11-SEP-1993; 93EP-00114631.

XX PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

XX Katinger H, Muster T;

XX

DR WPI; 1995-123428/16.

XX New peptide(s) corresponding to a HIV-1 gp 160 epitope - used to elicit
PT antibodies which neutralise different HIV-1 strains and inhibit cell
PT fusion caused by HIV-1.

XX Example 5; Page 15; 28pp; English.

XX Chimeric hemagglutinins carrying extended human MAb 2F5 epitopes
CC (AAR71631-36) were expressed by recombinant baculovirus in Sf9 cells. The
CC antibody response of mice immunized by these Sf9 cells was tested using
CC the peptide given in AAR71637 as a control. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX Sequence 9 AA;

Query Match 100.0%; Score 35; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

Qy 1 ELDKWA 6
|||||
Db 4 ELDKWA 9

RESULT 45

AAW99914

ID AAW99914 standard; peptide; 9 AA.

XX AC AAW99914;

XX DT 05-MAY-1999 (first entry)

XX DE HIV-1 vaccine synthetic peptide #3.

XX HIV-1; human immunodeficiency virus; vaccine; T-cell epitope;
KW gag protein; B-cell epitope; gp41 protein; chimeric; infection.

XX Synthetic.

XX Human immunodeficiency virus 1.

XX US5876731-A.

XX PD 02-MAR-1999.

XX PF 05-JUN-1995; 95US-00462507.

XX PR 09-JUN-1993; 93US-00073378.

XX PR 09-JUN-1994; 94US-00257528.

XX PA (CONN-) CONNAUGHT LAB LTD.

XX Chong P, Klein MH, Sia CDY;

XX WPI; 1999-189590/16.

XX Synthetic chimeric HIV polypeptides - comprising gag protein T-cell
PT epitope linked to gp41 B-cell epitope.

XX Claim 7; Col 72; 41pp; English.

XX The present invention describes a synthetic peptide comprising an amino
CC acid sequence containing a T-cell epitope of an HIV gag protein linked at
CC its C terminus to an amino acid sequence containing a B-cell epitope of
CC an HIV gp41 protein and containing the amino acid sequence: xLKDMWx2;
CC where X1 = E, A, G or Q, and X2 = A or T, or an amino acid sequence
CC capable of eliciting an HIV-specific antiserum and recognizing the
CC sequence xLKDMWx2. The synthetic peptide is useful in vaccines against
CC HIV infection and in diagnostic applications. AAW98892 to AAW98906, and
CC AAW98899 to AAW98989 represent synthetic peptides from the present
CC invention

XX Sequence 9 AA;

XX

Best Local Similarity 100.0%; Score 35; DB 2; Length 9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
 |||||
 Db 4 ELDKWA 9

Query Match 100.0%; Score 35; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
 |||||
 Db 4 ELDKWA 9

RESULT 47
 ABP15290
 ID ABP15290 standard; peptide; 9 AA.
 XX
 AC ABP15290;
 XX
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A24 super motif env peptide #170.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HW;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 182; 448pp; English.

Query Match 100.0%; Score 35; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
 |||||
 Db 4 ELDKWA 9

RESULT 46
 ABP20096
 ID ABP20096 standard; peptide; 9 AA.
 XX
 AC ABP20096;
 XX
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A03 motif env peptide #300.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HW;
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 281; 448pp; English.

The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

Query Match 100.0%; Score 35; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
 |||||
 Db 4 ELDKWA 9

Sequence 9 AA;
 Query Match 100.0%; Score 35; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 9 AA;
 Query Match 100.0%; Score 35; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)

Sequence 9 AA;
 Query Match 100.0%; Score 35; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 9 AA;
 Query Match 100.0%; Score 35; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 48
ABP12211
ID ABP12211 standard; peptide; 9 AA.
XX
AC ABP12211;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A02 super motif env peptide #268.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PR (EPIM-) EPIMMUNE INC.
XX
PA Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 119; 449pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 35; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 49
ABP18573
ID ABP18573 standard; peptide; 9 AA.
XX
AC ABP18573;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV BG2 super motif env peptide #148.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PR (EPIM-) EPIMMUNE INC.
XX
PA Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 249; 440pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 35; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

```

RESULT 50
AAB38721
ID AAB38721 standard; peptide; 10 AA.
XX
AC AAB38721;
XX
DT 02-FEB-2001 (first entry)
XX
DE HIV-1 peptide epitope #74.
XX
KW Vaccine; anti-HIV; HIV envelope protein; HIV infection.
XX
OS Human immunodeficiency virus.
XX
PW WO200058438-A2.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-US008232.
XX
PR 29-MAR-1999; 99US-0126938P.
XX
PA (BERN/) BERNSTEIN D.
PA (CHOW/) CHOWDHURY A.
PA (KOZH/) KOZHICH A.
PA (MOTS/) MOTSENBOCKER M.
XX
PI Bernstein D, Chowdhury A, Kozhich A, Motsenbocker M;
XX
DR WPI; 2000-656164/63.
XX
DT Synthetic peptides useful for preventing and treating HIV infection in
PT mammals, comprising a conformationally constrained portion and a portion
PT with continuous stretch of amino acids of predicted secondary structure.
XX
PS Disclosure; Page 11; 69pp; English.
XX
CC The present invention relates to peptides (AAB38648-B38970) comprising a
CC first conformationally constrained portion with a cross-linked group of a
CC HIV envelope protein that induces neutralising antibodies, and a second
CC portion comprising a continuous stretch of at least 5 amino acids having
CC a predicted secondary structure. The present sequence is one such
CC peptide. The peptides of the present invention are useful as a vaccine
CC for prophylactic or therapeutic treatment of a mammal for HIV infection
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 35; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.6; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
Db 3 ELDKWA 8
Search completed: March 16, 2004, 09:16:28
Job time : 62 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2004, 09:12:35 ; Search time 21 Seconds
(without alignments)
27.483 Million cell updates/sec

Title: US-10-024-329-2

Perfect score: 35

Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	357	2 S21994	envelope protein g
2	35	100.0	357	2 S21996	envelope protein g
3	35	100.0	357	2 S21992	envelope protein g
4	35	100.0	358	2 S21998	envelope protein g
5	35	100.0	443	2 A41621	env polypeptide M
6	35	100.0	445	2 A41621	env polypeptide M
7	35	100.0	464	2 S59898	kynureninase (EC 3
8	35	100.0	464	2 T48675	kynureninase (EC 3
9	35	100.0	465	2 G02652	kynureninase (EC 3
10	35	100.0	817	2 T16409	hypothetical prote
11	35	100.0	846	1 VCLJND	env polypeptide pr
12	35	100.0	847	2 T09448	envelope glycoprot
13	35	100.0	847	2 S13289	env protein - huma
14	35	100.0	851	2 S33985	env polypeptide -
15	35	100.0	852	1 VCLJBR	env polypeptide -
16	35	100.0	852	2 T12016	envelope glycoprot
17	35	100.0	853	2 S54384	envelope polypept
18	35	100.0	854	1 S13288	env protein - huma
19	35	100.0	855	1 VCLJAJ	env polypeptide pr
20	35	100.0	855	1 VCLJZR	env polypeptide pr
21	35	100.0	856	1 VCLJH3	env polypeptide pr
22	35	100.0	856	1 VCLJVL	env polypeptide pr
23	35	100.0	856	1 VCLJ3W	env polypeptide pr
24	35	100.0	859	1 VCLJWN	env polypeptide pr
25	35	100.0	859	2 T01672	envelope polypept
26	35	100.0	861	1 VCLJIV	env polypeptide pr
27	35	100.0	861	1 VCLJSC	env polypeptide pr
28	35	100.0	926	1 RDSFNH	nitrate reductase
29	32	91.4	268	2 T02448	hypothetical prote

30	32	91.4	326	2 E71561	probable solute pr
31	32	91.4	332	2 D71274	probable prolipid
32	32	91.4	448	2 C83347	probable dipeptida
33	32	91.4	501	2 S51160	nitrate reductase
34	32	91.4	617	2 S19254	nitrate reductase
35	32	91.4	868	1 VCLJTH	env polypeptide -
36	32	91.4	889	2 T02240	nitrate reductase
37	32	91.4	912	1 RDBHNS	nitrate reductase
38	32	91.4	915	1 RDBHNS	nitrate reductase
39	32	91.4	916	2 S07554	nitrate reductase
40	32	91.4	1707	2 S77910	hypothetical prote
41	32	88.6	78	2 E82798	hypothetical prote
42	31	88.6	112	2 C64746	yafu protein - Esc
43	31	88.6	126	2 H70387	hypothetical prote
44	31	88.6	151	2 AB0550	conserved hypothet
45	31	88.6	152	2 AH0368	conserved hypothet
46	31	88.6	201	2 A45332	zipper protein - c
47	31	88.6	229	2 AF1167	ABC transporter, A
48	31	88.6	248	2 B83030	probable rRNA meth
49	31	88.6	338	2 T33683	hypothetical prote
50	31	88.6	343	2 T20280	hypothetical prote
51	31	88.6	358	2 S22002	envelope protein g
52	31	88.6	358	2 S22000	envelope protein g
53	31	88.6	358	2 S70417	envelope protein g
54	31	88.6	392	2 B98080	galactokinase (EC
55	31	88.6	392	2 D95216	galactokinase (limp
56	31	88.6	418	2 JC7872	stearyl-CoA 9-des
57	31	88.6	483	2 A11908	hypothetical prote
58	31	88.6	500	1 A44001	gag polypeptide -
59	31	88.6	502	1 F0VWA2	gag polypeptide -
60	31	88.6	564	2 F59092	hypothetical prote
61	31	88.6	573	2 T05328	hypothetical prote
62	31	88.6	706	2 AD0173	conserved hypothet
63	31	88.6	719	2 T52510	hypothetical prote
64	31	88.6	733	2 S76856	hypothetical prote
65	31	88.6	745	2 B84673	hypothetical prote
66	31	88.6	752	2 F81203	maltoase phosphoryl
67	31	88.6	752	2 C81781	probable maltoase p
68	31	88.6	785	2 S73098	aminopeptidase (EC
69	31	88.6	826	2 E90289	malate synthase, p
70	31	88.6	854	1 VCLJSI	env polypeptide pr
71	31	88.6	863	2 A53034	gag polypeptide -
72	31	88.6	877	2 S45197	envelope protein p
73	31	88.6	880	1 SYBSVS	valine-tRNA ligase
74	31	88.6	881	2 S25445	nitrate reductase
75	31	88.6	884	2 S66308	nitrate reductase
76	31	88.6	886	2 A59223	nitrate reductase
77	31	88.6	1022	2 I53078	homeotic gene regu
78	31	88.6	1055	1 A37205	leukotoxin A - Act
79	31	88.6	1235	1 VGIHMJ	E2 glycoprotein pr
80	31	88.6	1257	2 T28937	hypothetical prote
81	31	88.6	1324	1 VGIH59	E2 glycoprotein pr
82	31	88.6	1376	1 VGIHJ2	E2 glycoprotein pr
83	31	88.6	1376	1 JQ1534	E2 glycoprotein pr
84	31	88.6	1572	2 S45251	SNFalpha protein
85	31	88.6	1586	2 S39580	HBRM protein - hum
86	31	88.6	1613	2 S39059	protein BRG1 - hum
87	31	88.6	1647	2 S45252	SNF2beta protein -
88	30	85.7	120	2 F96658	hypothetical prote
89	30	85.7	166	2 TS0531	hypothetical prote
90	30	85.7	167	2 S76890	hypothetical prote
91	30	85.7	314	2 T42604	probable uracil-DN
92	30	85.7	325	2 T03010	probable replicati
93	30	85.7	327	2 AF0618	conserved hypothet
94	30	85.7	336	2 PC1139	hypothetical prote
95	30	85.7	339	2 AC2153	hypothetical prote
96	30	85.7	357	2 S22006	envelope protein g
97	30	85.7	357	2 S22004	envelope protein g
98	30	85.7	430	2 S75701	hypothetical prote
99	30	85.7	433	2 T04594	aldehyde dehydroge
100	30	85.7	441	2 AE2976	agaE protein (limpo
101	30	85.7	441	2 F98306	agaE protein (limpo
102	30	85.7	448	2 D86368	hypothetical prote

103	30	85.7	478	2	T15516	hypothetical prote	176	28	80.0	109	2	C82413	pterin-4-alpha-car
104	30	85.7	568	2	S28089	hypothetical prote	177	28	80.0	139	2	S41579	lysozyme (EC 3.2.1
105	30	85.7	612	2	A49403	tetratricopeptide-	178	28	80.0	148	2	C90269	hypothetical prote
106	30	85.7	719	2	T30438	exoglucanase - Clo	179	28	80.0	152	2	A97090	hypothetical prote
107	30	85.7	775	2	T01712	subtilisin-like pr	180	28	80.0	154	2	D82795	phage-related endo
108	30	85.7	843	1	H44001	env polyprotein pr	181	28	80.0	155	2	H83146	conserved hypothet
109	30	85.7	856	1	JC5256	adipocyte transcri	182	28	80.0	155	2	D87399	cytochrome c famil
110	30	85.7	856	1	A44963	env polyprotein pr	183	28	80.0	162	2	E86762	hypothetical prote
111	30	85.7	891	1	RDBHNP	nitrate reductase	184	28	80.0	192	2	H96828	hypothetical prote
112	30	85.7	904	1	RDNTNT	nitrate reductase	185	28	80.0	192	2	C89153	protein C24B5.4 [i
113	30	85.7	904	1	RDNTNS	nitrate reductase	186	28	80.0	194	2	C84033	hypothetical prote
114	30	85.7	908	2	JN0665	nitrate reductase	187	28	80.0	197	2	AB3212	2-hydroxychromene-
115	30	85.7	940	2	C70152	isoleucine-TRNA li	188	28	80.0	200	2	F97055	probable nucleotid
116	30	85.7	1494	2	C84947	serine/choleoline k	189	28	80.0	200	2	D97224	probable GTPase, Y
117	30	85.7	2021	2	AD2267	sensory transducti	190	28	80.0	201	2	T51665	myb-related transc
118	30	85.7	2140	2	F95074	serine proteinase,	191	28	80.0	223	2	C70524	hypothetical prote
119	30	85.7	2144	2	A97942	metalloproteinase	192	28	80.0	229	2	AH1525	hypothetical prote
120	30	85.7	2528	2	T20719	hypothetical prote	193	28	80.0	274	2	D86300	ABC transporter, A
121	30	85.7	4910	2	S64942	probable membrane	194	28	80.0	280	2	D86889	hypothetical prote
122	29	82.9	130	2	T04048	hypothetical prote	195	28	80.0	281	2	H64125	zinc ABC transport
123	29	82.9	142	2	T51902	hypothetical prote	196	28	80.0	281	2	T52189	modD protein homol
124	29	82.9	154	2	G87571	hypothetical prote	197	28	80.0	283	2	C88469	ethylene responsiv
125	29	82.9	182	2	E87289	conserved hypothet	198	28	80.0	291	2	AI1828	protein C28H8.7 [i
126	29	82.9	255	2	AD1257	B. subtilis RecO p	199	28	80.0	325	2	T18283	hypothetical prote
127	29	82.9	259	2	C95849	conserved hypothet	200	28	80.0	329	2	G82243	conserved hypothet
128	29	82.9	260	2	T22792	hypothetical prote	201	28	80.0	339	2	T24725	hypothetical prote
129	29	82.9	261	2	S52609	hypothetical prote	202	28	80.0	362	2	A10370	probable exported
130	29	82.9	275	2	B75479	conserved hypothet	203	28	80.0	370	1	D22930	DNA repair and gen
131	29	82.9	283	2	S06183	repressor protein	204	28	80.0	372	1	S76448	translation releas
132	29	82.9	283	2	S06182	transcription regu	205	28	80.0	377	1	S01615	site-specific DNA-
133	29	82.9	284	2	AC2944	hypothetical prote	206	28	80.0	379	2	B07777	hypothetical prote
134	29	82.9	285	2	G72414	probable transcrip	207	28	80.0	405	2	AE2197	ABC transporter, m
135	29	82.9	287	2	G98338	probable polynucle	208	28	80.0	407	2	AC0971	DNA/pantothenate m
136	29	82.9	295	2	B83587	hypothetical prote	209	28	80.0	407	2	AC0971	conserved hypothet
137	29	82.9	311	2	D85631	hypothetical prote	210	28	80.0	430	1	A65165	hypothetical prote
138	29	82.9	326	2	F81714	ABC transporter, p	211	28	80.0	430	2	T24273	pantothenate metab
139	29	82.9	348	2	T17304	hypothetical prote	212	28	80.0	430	2	B91193	pantothenate metab
140	29	82.9	367	2	A70550	probable pdhA prot	213	28	80.0	445	2	H88244	protein T01B7.5 [i
141	29	82.9	379	2	G82402	conserved hypothet	214	28	80.0	454	2	S01092	fodrin alpha chain
142	29	82.9	388	2	H85692	hypothetical prote	215	28	80.0	454	2	S01092	hypothetical prote
143	29	82.9	391	2	C90908	probable host spec	216	28	80.0	457	2	E86080	chemotaxis protein
144	29	82.9	391	2	H90968	probable host spec	217	28	80.0	457	2	E91233	two-component sens
145	29	82.9	391	2	H90996	probable host spec	218	28	80.0	457	2	S40855	protein F46F5.7 [i
146	29	82.9	401	2	G82737	argininosuccinate	219	28	80.0	457	2	AD0943	hypothetical prote
147	29	82.9	470	2	B96741	hypothetical prote	220	28	80.0	465	2	H88029	gag polyprotein -
148	29	82.9	492	2	T36429	probable iron-sulf	221	28	80.0	476	2	T29463	cation ABC transpo
149	29	82.9	494	1	VCCVCE	coat protein - car	222	28	80.0	478	1	FOVWVL	gag polyprotein -
150	29	82.9	651	2	F89798	hypothetical prote	223	28	80.0	490	2	H69858	gag polyprotein -
151	29	82.9	671	2	B75607	conserved hypothet	224	28	80.0	500	1	FOVWLV	hypothetical prote
152	29	82.9	808	2	T04092	phospholipase D (E	225	28	80.0	500	1	FOVWLV	hypothetical prote
153	29	82.9	809	2	T11695	phospholipase D (E	226	28	80.0	502	2	T19708	gag polyprotein -
154	29	82.9	812	2	T03659	phospholipase D (E	227	28	80.0	506	1	A38068	gag polyprotein -
155	29	82.9	890	2	T11805	nitrate reductase	228	28	80.0	512	1	FOVWH3	gag polyprotein -
156	29	82.9	898	1	RDBJNH	nitrate reductase	229	28	80.0	513	2	S62000	probable membrane
157	29	82.9	900	2	S47029	nitrate reductase	230	28	80.0	533	2	D83014	conserved hypothet
158	29	82.9	900	2	A95340	cation transport P	231	28	80.0	533	2	T23419	hypothetical prote
159	29	82.9	911	1	RDTONH	nitrate reductase	232	28	80.0	535	2	G69074	formylmethanofuran
160	29	82.9	918	2	A41667	nitrate reductase	233	28	80.0	569	2	S57456	formylmethanofuran
161	29	82.9	920	2	S52301	nitrate reductase	234	28	80.0	571	2	C70353	succinate dehydrog
162	29	82.9	977	2	D85741	nitrate reductase	235	28	80.0	573	2	C86806	hypothetical prote
163	29	82.9	1132	1	QSBPL	hypothetical prote	236	28	80.0	603	2	EJ1444	probable EREBP-4 -
164	29	82.9	1132	2	H90834	host specificity p	237	28	80.0	620	2	JH0593	Schwann cell myeli
165	29	82.9	1137	2	B90734	host specificity p	238	28	80.0	623	2	A70741	hypothetical prote
166	29	82.9	1138	2	D85584	probable host spec	239	28	80.0	660	2	C86877	hypothetical prote
167	29	82.9	1149	2	T20891	probable tail comp	240	28	80.0	662	2	T47649	hypothetical prote
168	29	82.9	1157	2	A90769	probable host spec	241	28	80.0	688	2	T23108	hypothetical prote
169	29	82.9	1158	2	F90854	probable tail comp	242	28	80.0	749	2	A99438	hypothetical prote
170	29	82.9	1158	2	G85718	probable host spec	243	28	80.0	762	2	G88436	protein T04A8.13 [
171	29	82.9	1159	2	A90899	hypothetical prote	244	28	80.0	765	2	AD3549	diguanilate cyclas
172	29	82.9	1159	2	G85916	hypothetical prote	245	28	80.0	791	2	T24435	hypothetical prote
173	29	82.9	1165	2	F90877	probable host spec	246	28	80.0	791	1	RDMUNH	nitrate reductase
174	29	82.9	1165	2	D85842	probable tail fibe	247	28	80.0	938	2	T51422	hypothetical prote
175	29	82.9	1337	2	T38949	hypothetical prote	248	28	80.0				

249	28	80.0	950	2	T28793	diacylglycerol kin	322	27	77.1	301	2	T20651	hypothetical prote
250	28	80.0	952	2	T28792	diacylglycerol kin	323	27	77.1	303	2	S77235	hypothetical prote
251	28	80.0	956	2	B71250	valine-tRNA ligase	324	27	77.1	306	2	B69992	ABC transporter (m
252	28	80.0	957	2	H69141	hypothetical prote	325	27	77.1	306	2	T06042	hypothetical prote
253	28	80.0	1004	2	A39611	probable GTP-bind	326	27	77.1	309	1	PAHU2A	phosphoprotein pho
254	28	80.0	1108	2	T35827	probable membrane	327	27	77.1	309	1	A27430	phosphoprotein pho
255	28	80.0	1252	2	A47213	beta-fodrin - huma	328	27	77.1	309	1	S10371	phosphoprotein pho
256	28	80.0	1272	2	T30248	fragile X mental r	329	27	77.1	309	1	PABBA1	phosphoprotein pho
257	28	80.0	1297	2	S25714	son-of-sevenless-2	330	27	77.1	309	1	PART2A	phosphoprotein pho
258	28	80.0	1323	1	RRWGS	RNA-directed RNA p	331	27	77.1	309	1	S20348	phosphoprotein pho
259	28	80.0	1333	2	A37488	Ras guanine nucleo	332	27	77.1	309	1	PAHU2B	phosphoprotein pho
260	28	80.0	1336	2	S25716	Ras guanine nucleo	333	27	77.1	309	1	PARB2B	phosphoprotein pho
261	28	80.0	1407	1	T00558	probable ABC trans	334	27	77.1	309	1	PART2B	phosphoprotein pho
262	28	80.0	1408	2	T47671	P-glycoprotein-Lik	335	27	77.1	309	1	JC4316	phosphoprotein pho
263	28	80.0	1436	2	JC5290	protein-tyrosine-p	336	27	77.1	309	2	T17557	phosphoprotein pho
264	28	80.0	1442	2	S72441	protein-tyrosine-p	337	27	77.1	320	1	A05023	procyclin homolog
265	28	80.0	1495	2	E86428	probable ABC trans	338	27	77.1	323	1	R84423	cytochrome c-type
266	28	80.0	1707	2	S77908	hypothetical prote	339	27	77.1	324	2	D72070	hypothetical prote
267	28	80.0	1811	2	T00035	nonstructural poly	340	27	77.1	324	2	B86555	conserved hypoteth
268	28	80.0	2228	2	E97942	beta-galactosidase	341	27	77.1	325	2	A28029	Crz9 hypothetical
269	28	80.0	2233	2	B95075	beta-galactosidase	342	27	77.1	325	2	G83921	phosphoprotein pho
270	28	80.0	2364	1	A44159	spectrin beta-G ch	343	27	77.1	327	2	T36304	hypothetical prote
271	28	80.0	3603	1	D69681	peptide synthetase	344	27	77.1	335	2	B97190	probable anthranil
272	28	80.0	3712	1	YGCEVC	alpha-aminoadipyl-	345	27	77.1	336	2	B87475	hypothetical prote
273	27	77.1	53	2	C82776	hypothetical prote	346	27	77.1	336	2	S35068	DNA polymerase III
274	27	77.1	64	1	QABP22	restriction inhibi	347	27	77.1	339	2	T37207	hypothetical prote
275	27	77.1	65	2	S76998	hypothetical prote	348	27	77.1	342	2	B82418	L-allo-threonine a
276	27	77.1	66	1	QABPL	restriction inhibi	349	27	77.1	343	2	R84773	hypothetical prote
277	27	77.1	76	2	S10068	restriction inhibi	350	27	77.1	347	2	T08327	hypothetical prote
278	27	77.1	100	2	C72690	hypothetical prote	351	27	77.1	348	2	S44628	f22b7.1 protein -
279	27	77.1	102	2	F97004	probable transcrip	352	27	77.1	348	2	JQ2327	Alu protein - Indi
280	27	77.1	107	2	A81995	hypothetical prote	353	27	77.1	351	2	F83914	hypothetical prote
281	27	77.1	115	2	AF1366	transcription regu	354	27	77.1	355	2	A72317	alcohol dehydrogen
282	27	77.1	115	2	AG1735	transcription regu	355	27	77.1	359	2	H75466	lipopolyaaccharide
283	27	77.1	120	2	A80398	probable sigma 54	356	27	77.1	364	2	T20652	hypothetical prote
284	27	77.1	124	2	C87842	hypothetical prote	357	27	77.1	365	2	D75096	aspartate aminotra
285	27	77.1	125	2	F81234	conserved hypoteth	358	27	77.1	366	2	T24620	hypothetical prote
286	27	77.1	126	2	F82008	hypothetical prote	359	27	77.1	369	2	A96927	probable N6-adenin
287	27	77.1	131	2	B30900	probable minor tai	360	27	77.1	373	2	T40864	hypothetical prote
288	27	77.1	140	2	S41573	lysozyme (EC 3.2.1	361	27	77.1	381	2	B97182	acyl-protein synth
289	27	77.1	144	2	D83209	hypothetical prote	362	27	77.1	381	2	B47013	butanol dehydrogen
290	27	77.1	145	2	G84148	hypothetical prote	363	27	77.1	390	2	D97305	NADH-dependent but
291	27	77.1	146	2	D95092	conserved hypoteth	364	27	77.1	390	2	H90421	hypothetical prote
292	27	77.1	146	2	A37960	conserved hypoteth	365	27	77.1	395	2	B90459	FIXC protein homol
293	27	77.1	162	2	D84684	hypothetical prote	366	27	77.1	396	2	F84326	GTP-binding protei
294	27	77.1	163	1	BRAD21	early E1B 19K prot	367	27	77.1	399	2	A82351	DNA/pantothenate m
295	27	77.1	192	2	C64767	yail protein - Esc	368	27	77.1	399	2	G64104	pantothenate metab
296	27	77.1	192	2	E80683	hypothetical prote	369	27	77.1	400	2	T19390	hypothetical prote
297	27	77.1	192	2	A85534	hypothetical prote	370	27	77.1	402	2	H90222	GRP binding protei
298	27	77.1	192	2	G97754	hypothetical prote	371	27	77.1	408	2	D64216	hypothetical prote
299	27	77.1	195	2	AC2527	hypothetical prote	372	27	77.1	412	2	AB1000	type II secretion
300	27	77.1	197	2	B83485	probable transcrip	373	27	77.1	414	2	AG2407	site-specific DNA-
301	27	77.1	208	2	I64209	ribosomal protein	374	27	77.1	423	2	D96552	unknown protein, 7
302	27	77.1	214	2	H84981	hypothetical prote	375	27	77.1	427	2	G83764	diaminobutyric aci
303	27	77.1	230	2	AG0931	conserved hypoteth	376	27	77.1	427	2	S04020	hypothetical prote
304	27	77.1	233	2	T48179	hypothetical prote	377	27	77.1	437	2	T03878	hypothetical prote
305	27	77.1	236	2	B56281	7alpha-cephen-meth	378	27	77.1	441	2	S73996	MG148 homolog Vxps
306	27	77.1	236	2	E70028	conserved hypoteth	379	27	77.1	445	2	A47676	bacteriocin 28b -
307	27	77.1	237	2	T21376	hypothetical prote	380	27	77.1	449	2	B41621	env polypeptin D
308	27	77.1	240	2	E84390	sterol C-methyl	381	27	77.1	454	2	G82083	glutamate synthase
309	27	77.1	243	2	A26599	clathrin light cha	382	27	77.1	471	2	G75255	probable magnesium
310	27	77.1	247	2	T32859	hypothetical prote	383	27	77.1	487	2	AC1856	diaminobutyrate-py
311	27	77.1	248	2	E82892	conserved hypoteth	384	27	77.1	493	2	T09436	gag polyprotein -
312	27	77.1	255	2	T06587	acid phosphatase (385	27	77.1	498	2	T46161	glucosyltransferas
313	27	77.1	264	2	A54060	nicotinamide N-met	386	27	77.1	507	2	A47436	1,25-dihydroxyvita
314	27	77.1	268	2	A52363	inositol monophosp	387	27	77.1	514	1	S60033	25-hydroxyvitamin
315	27	77.1	271	2	C47127	tetracenomycin C s	388	27	77.1	514	2	A45228	25-hydroxyvitamin
316	27	77.1	271	2	E83942	hypothetical prote	389	27	77.1	522	2	A46103	transmembrane glyc
317	27	77.1	276	2	A81095	hypothetical prote	390	27	77.1	522	2	A35149	ipah protein - Shi
318	27	77.1	278	2	AS1458	hypothetical prote	391	27	77.1	532	2	C97765	CTP synthase (EC 6
319	27	77.1	281	2	T30596	hypothetical prote	392	27	77.1	537	2	T38927	hypothetical prote
320	27	77.1	290	2	A82687	conserved hypoteth	393	27	77.1	539	2	A82320	methy1-accepting c
321	27	77.1	292	1	E64226	hypothetical prote	394	27	77.1	541	2	B86264	hypothetical prote

395	27	77.1	556	1	S10901	choline dehydrogen
396	27	77.1	557	2	S25023	neurofilament-like
397	27	77.1	561	2	A84113	transposase (12) B
398	27	77.1	561	2	T19604	hypothetical prote
399	27	77.1	562	2	E90673	choline dehydrogen
400	27	77.1	562	2	A85524	malate oxidoreduct
401	27	77.1	565	2	S44330	hypothetical prote
402	27	77.1	571	2	T27220	hypothetical prote
403	27	77.1	571	2	S37913	ipAH protein - Shi
404	27	77.1	574	2	A35810	alpha,alpha-trehal
405	27	77.1	586	2	C71695	ctp synthase (pyrG
406	27	77.1	593	2	B81277	hypothetical prote
407	27	77.1	598	2	H86460	hypothetical prote
408	27	77.1	603	2	T00379	KIAA0640 protein -
409	27	77.1	605	2	AG0460	probable carbon st
410	27	77.1	612	2	T05331	hypothetical prote
411	27	77.1	619	2	S67067	probable membrane
412	27	77.1	628	2	S37795	hypothetical prote
413	27	77.1	630	2	E71451	hypothetical prote
414	27	77.1	632	2	B75215	5'-adenylylphospho
415	27	77.1	633	2	G96503	protein P9C16.15 [
416	27	77.1	634	2	S75962	NADH2 dehydrogenas
417	27	77.1	636	2	T51893	related to Che-1 p
418	27	77.1	644	2	G85072	hypothetical prote
419	27	77.1	644	2	C85944	probable oxidoredu
420	27	77.1	644	2	G91098	probable oxidoredu
421	27	77.1	649	2	C81275	hypothetical prote
422	27	77.1	651	2	S65296	hypothetical prote
423	27	77.1	653	2	B81277	hypothetical prote
424	27	77.1	684	2	T40319	hypothetical prote
425	27	77.1	694	2	A69768	transcription anti
426	27	77.1	702	2	AH0625	conserved hypothet
427	27	77.1	716	2	T01802	hypothetical prote
428	27	77.1	718	2	E71100	hypothetical prote
429	27	77.1	723	2	H82035	fatty oxidation co
430	27	77.1	751	2	T31515	hypothetical prote
431	27	77.1	756	2	T20109	hypothetical prote
432	27	77.1	789	2	A88395	protein P53A3.2 [i
433	27	77.1	812	2	E97831	valine-tRNA ligase
434	27	77.1	822	2	F68812	phosphoketotolase [i
435	27	77.1	851	2	AD0407	DNA mismatch repair
436	27	77.1	853	2	A28668	DNA mismatch repair
437	27	77.1	853	2	I54964	DNA mismatch repair
438	27	77.1	853	2	E91077	MutS protein [impo
439	27	77.1	853	2	F85922	methyl-directed mi
440	27	77.1	853	2	AB2020	hypothetical prote
441	27	77.1	853	2	AB2020	DNA mismatch repair
442	27	77.1	855	2	AH0853	DNA mismatch repair
443	27	77.1	861	2	G64087	DNA mismatch repair
444	27	77.1	862	2	B82312	DNA mismatch repair
445	27	77.1	868	2	S64747	probable membrane
446	27	77.1	876	2	AC2914	leucyl-tRNA synthet
447	27	77.1	876	2	F97688	leucyl-tRNA synthet
448	27	77.1	882	2	AB1631	valyl-tRNA synthet
449	27	77.1	883	2	AH1268	valyl-tRNA synthet
450	27	77.1	902	2	D83467	probable cation-tr
451	27	77.1	902	2	S26002	gene coxI intron 1
452	27	77.1	903	2	T26743	hypothetical prote
453	27	77.1	908	2	T22376	hypothetical prote
454	27	77.1	925	1	SYECIT	regulatory protein
455	27	77.1	938	1	E90673	isoleucine-tRNA li
456	27	77.1	938	2	E90673	isoleucine-tRNA sy
457	27	77.1	938	2	D85483	isoleucine-tRNA sy
458	27	77.1	941	2	S78633	isoleucine-tRNA li
459	27	77.1	943	2	B83077	isoleucyl-tRNA syn
460	27	77.1	944	2	AI0507	isoleucyl-tRNA syn
461	27	77.1	949	2	D82293	isoleucyl-tRNA syn
462	27	77.1	951	2	T26738	hypothetical prote
463	27	77.1	975	2	T26737	hypothetical prote
464	27	77.1	1024	2	T41415	probable leucine p
465	27	77.1	1031	2	D88312	protein T06A10.1 [
466	27	77.1	1031	2	T33655	hypothetical prote
467	27	77.1	1037	2	F82171	transporter, AcrB/

468	27	77.1	1066	2	T30903	arachidonate 8-lip
469	27	77.1	1139	2	S40932	hypothetical prote
470	27	77.1	1148	2	A28614	nonstructural poly
471	27	77.1	1159	2	T15963	hypothetical prote
472	27	77.1	1161	2	I59311	nardilysin (SC 3.4
473	27	77.1	1179	2	T04584	TMV resistance pro
474	27	77.1	1188	2	T20333	hypothetical prote
475	27	77.1	1353	1	JQ2168	E2 glycoprotein pr
476	27	77.1	1359	2	A98883	nuclear protein ST
477	27	77.1	1361	2	S29998	surface protein -
478	27	77.1	1362	2	A37474	surface glycoprote
479	27	77.1	1363	1	VG1HNM	E2 glycoprotein pr
480	27	77.1	1363	1	VG1HQU	E2 glycoprotein pr
481	27	77.1	1363	1	VG1HFI	E2 glycoprotein pr
482	27	77.1	1363	1	VG1HL9	E2 glycoprotein pr
483	27	77.1	1363	1	VG1HVA	E2 glycoprotein pr
484	27	77.1	1363	1	VG1HLY	surface protein -
485	27	77.1	1363	2	S44240	surface protein -
486	27	77.1	1363	2	S44241	myosin-like protei
487	27	77.1	1374	2	D85390	myosin heavy chain
488	27	77.1	1375	2	T05200	DNA polymerase III
489	27	77.1	1443	2	S73446	hypothetical prote
490	27	77.1	1490	2	T20513	hypothetical prote
491	27	77.1	1494	2	T28452	myosin MYAI, class
492	27	77.1	1520	2	S46444	probable membrane
493	27	77.1	1559	1	S64757	transcription acti
494	27	77.1	1638	2	A42091	probable transcrip
495	27	77.1	1680	2	T17272	hypothetical prote
496	27	77.1	1780	2	T17272	myosin heavy chain
497	27	77.1	1968	1	S05697	receptor tyrosine
498	27	77.1	2051	2	T30938	tiggrin - fruit fl
499	27	77.1	2186	2	T13169	hypothetical prote
500	27	77.1	2331	2	T25410	hypothetical prote

ALIGNMENTS

RESULT 1

S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21994; S70421
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebra
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>
A:Cross-references: EMBL:X61355; NID:g60179
C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6

Db 163 ELDKWA 168

RESULT 2

S21996
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by phylogenetic analysis
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70422
 A:Molecule type: DNA
 A:Residues: 1-357 <ST2>
 A:Cross-references: EMBL:X61358; NID:G60182; PIDN:CAA43630.1; PID:G60183
 A:Experimental source: patient 27L
 A:Note: submitted to the EMBL Data Library, July 1991
 C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||

Db 163 ELDKWA 168

RESULT 3

S21992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by phylogenetic analysis
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70424
 A:Molecule type: DNA
 A:Residues: 1-357 <ST2>
 A:Cross-references: EMBL:X61358; NID:G60177; PIDN:CAA43628.1; PID:G60178
 A:Experimental source: patient 22
 A:Note: submitted to the EMBL Data Library, July 1991
 C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||

Db 163 ELDKWA 168

RESULT 4

S21998
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by phylogenetic analysis
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S21998; S70425
 A:Molecule type: DNA
 A:Residues: 1-358 <ST1>
 A:Cross-references: EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:G60183
 A:Experimental source: patient 27L
 A:Note: submitted to the EMBL Data Library, July 1991
 C:Superfamily: type E retrovirus env polyprotein

Qy 1 ELDKWA 6
 |||||

Db 163 ELDKWA 168

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by phylogenetic analysis
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70425
 A:Molecule type: DNA
 A:Residues: 1-358 <ST2>
 A:Cross-references: EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:G60183
 A:Experimental source: patient 27L
 A:Note: submitted to the EMBL Data Library, July 1991
 C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 358;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||

Db 164 ELDKWA 169

RESULT 5

C41621
 A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
 A:Reference number: A41621; MUID:92107924; PMID:1763038
 A:Accession: C41621
 A:Molecule type: DNA
 A:Residues: 1-443 <BUR>
 A:Cross-references: GB:M77230; NID:G328631; PIDN:AA03792.1; PID:G555013
 A:Note: this virus was isolated from the mother's sexual partner
 C:Genetics: env
 A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
 F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
 F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
 F:424-443/Domain: transmembrane #status predicted <TMN>
 F:9-23-36-48-78-101-107-131-137-143-147-153-188-200-203-351-356-377/Binding site: ca

Query Match 100.0%; Score 35; DB 2; Length 443;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||

Db 402 ELDKWA 407

RESULT 6

A41621
 A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
 A:Reference number: A41621; MUID:92107924; PMID:1763038
 A:Accession: A41621
 A:Molecule type: DNA
 A:Residues: 1-445 <BUR>
 A:Cross-references: GB:M77228; NID:G328627; PIDN:AA03790.1; PID:G555013
 A:Note: this virus was isolated from the mother
 C:Genetics: env
 A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
 F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
 F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
 F:424-443/Domain: transmembrane #status predicted <TMN>
 F:9-23-36-48-78-101-107-131-137-143-147-153-188-200-203-351-356-377/Binding site: ca

Query Match 100.0%; Score 35; DB 2; Length 443;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||

Db 402 ELDKWA 407

A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F;1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;426-445/Domain: transmembrane #status predicted <TM>
F;9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:

Query Match 100.0%; Score 35; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
DB 404 ELDKWA 409

RESULT 7
S59898
Kynureninase (EC 3.7.1.3) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S59898
R;Takeuchi, F.; Tsubouchi, R.; Yoshino, M.; Shibata, Y.
Biochim. Biophys. Acta 1252, 185-188, 1995
A:Title: Amino-acid sequence of rat liver kynureninase.
A:Reference number: S59898; MUID:96049498; PMID:7578221
A:Accession: S59898
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-464 <TA>
C:Keywords: hydrolase

Query Match 100.0%; Score 35; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
DB 90 ELDKWA 95

RESULT 8
T48675
kynureninase (EC 3.7.1.3) [validated] - rat
N:Alternate names: L-kynurenine hydrolase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 21-Jul-2000
C:Accession: T48675
R;Toma, S.; Nakamura, M.; Tone, S.; Okuno, E.; Kido, R.; Breton, J.; Avanzi, N.; Cozzi, F.EBS Lett. 408, 5-10, 1997
A:Title: Cloning and recombinant expression of rat and human kynureninase.
A:Reference number: Z24527; MUID:97324088; PMID:9180257
A:Accession: T48675
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-464 <TM>
A:Cross-references: EMBL:U68168; NID:g1532215; PIDN:AAC53206.1; PID:g1532216
A:Experimental source: liver
C:Function:
A:Description: EC 3.7.1.3 [validated, MUID:97324088]
A:Pathway: biosynthesis of NAD cofactors
C:Keywords: hydrolase

Query Match 100.0%; Score 35; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
DB 90 ELDKWA 95

RESULT 9
G02652
Kynureninase (EC 3.7.1.3) - human
N:Alternate names: L-kynurenine hydrolase
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: G02652
R;Malherbe, P.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01539
A:Accession: G02652
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-465 <MAL>
A:Cross-references: EMBL:U57721; NID:g1323714; PIDN:AAC50650.1; PID:g1323715
C:Keywords: hydrolase

Query Match 100.0%; Score 35; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
DB 90 ELDKWA 95

RESULT 10
T16409
hypothetical protein F48E8.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16409
R;Kirsten, J.
submitted to the EMBL Data Library, March 1995
A:Description: The sequence of C. elegans cosmid F48E8.
A:Reference number: S59413
A:Accession: T16409
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-817 <KIR>
A:Cross-references: EMBL:U23514; NID:g746484; PID:g746490; PIDN:AAC46543.1; CESP:F48E8.6
A:Experimental source: strain Bristol N2
C:Genetics:

A:Gene: CESP:F48E8.6
A:Introns: 107/3; 510/3; 670/3; 733/3

Query Match 100.0%; Score 35; DB 2; Length 817;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
DB 359 ELDKWA 364

RESULT 11
VCLJND
env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: JQ0066
R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.; Gene 81, 275-284, 1989
A:Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunodeficiency virus type 1.
A:Reference number: JQ0065; MUID:90034200; PMID:2806917
A:Accession: JQ0066
A:Molecule type: DNA
A:Residues: 1-846 <SPI>
A:Cross-references: GB:M27323; NID:g328154; PIDN:AAA44873.1; PID:g328162
A:Note: the authors translated the codon GCG for residue 523 as Arg

C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <CP1>
F:502-846/Product: coat protein gp41 #status predicted <CP2>
F:502-520/Domain: transmembrane #status predicted <TM1>
F:674-692/Domain: transmembrane #status predicted <TM2>
F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

Query Match 100.0%; Score 35; DB 1; Length 846;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|
|
|
|
|
Db 652 ELDKWA 657

RESULT 12
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C;Accession: T09448
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
submitted to the EMBL Data Library, July 1996
A;Reference number: Z16673
A;Accession: T09448
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-847 <PAN>
A;Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|
|
|
|
|
Db 653 ELDKWA 658

RESULT 13
S13289
env protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S13289
R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A;Reference number: S13288; MUID:91043044; PMID:2172833
A;Accession: S13289
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-847 <ORR>
C;Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|
|
|
|
|
Db 653 ELDKWA 658

RESULT 14

S33985
env polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C;Accession: S33985
R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Accession: S33985
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-851 <CAR>
A;Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199
C;Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|
|
|
|
|
Db 657 ELDKWA 662

RESULT 15
VCLJBR
env polyprotein - human immunodeficiency virus type 1 (isolate BR)
N;Alternate names: coat polyprotein
C;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Feb-1997
R;Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S.
Virology 168, 79-89, 1989
A;Title: Biological and molecular characterization of human immunodeficiency virus (HIV-1)
A;Reference number: A94389; MUID:89085613; PMID:2789516
A;Accession: A31667
A;Molecule type: DNA
A;Residues: 1-852 <ANA>
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; polyprotein; transmembrane protein
F:1-516/Product: coat protein gp120 #status predicted <CP1>
F:517-852/Product: coat protein gp41 #status predicted <CP2>

Query Match 100.0%; Score 35; DB 1; Length 852;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|
|
|
|
|
Db 658 ELDKWA 663

RESULT 16
T12016
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T12016
R;McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A;Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
A;Reference number: Z17379; MUID:98178716; PMID:9519894
A;Accession: T12016
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-852 <MCC>
A;Cross-references: EMBL:U90934; NID:g2351783; PIDN:AAC59271.1; PID:g2351784
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein

Thu Mar 18 10:20:34 2004

```
Query Match      100.0%; Score 35; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
      |||||
Db      658 ELDKWA 663

RESULT 17
S54384
envelope polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C:Accession: S54384
R:Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A:Reference number: S54377
A:Accession: S54384
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-853 <THE>
A:Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA45370.1; PID:g329385
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: polyprotein

Query Match      100.0%; Score 35; DB 2; Length 853;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
      |||||
Db      659 ELDKWA 664

RESULT 18
S13288
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S13288
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OBR>
C:Superfamily: type E retrovirus env polyprotein

Query Match      100.0%; Score 35; DB 2; Length 854;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
      |||||
Db      660 ELDKWA 665

RESULT 19
VCLJAJ2
env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03976
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sh
Science 227, 484-492, 1985
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A:Reference number: A04003; MUID:85090453; PMID:2578227
A:Accession: A03976
```

```
A:Molecule type: DNA
A:Residues: 1-855 <SAN>
A:Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666
C:Genetics:
A:Gene: env
A:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>
F:510-855/Product: transmembrane glycoprotein #status predicted <TMM>
F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      100.0%; Score 35; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
      |||||
Db      661 ELDKWA 666

RESULT 20
VCLJZR
env polyprotein precursor - human immunodeficiency virus Zr-6
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus Zr-6
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C:Accession: D26192
R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti
A:Reference number: A26192; MUID:87248097; PMID:3036660
A:Accession: D26192
A:Molecule type: DNA
A:Residues: 1-855 <SRI>
A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-855/Product: env polyprotein #status predicted <MAT>
F:20-855/Product: exterior membrane glycoprotein #status predicted <EXT>
F:501-855/Product: transmembrane glycoprotein #status predicted <TMM>
F:87,129,140,145,154,158,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match      100.0%; Score 35; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
      |||||
Db      661 ELDKWA 666

RESULT 21
VCLJH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora
nberger, J.A.; Papas, T.S.; Graybe, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA44,
```

C;Genetics: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
 F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
 F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
 F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 856;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 662 ELDKWA 667

RESULT 22
 VCLJVL
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
 N;Alternate names: coat polyprotein
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
 C;Accession: A03974
 R;Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Laaky, L.A.; Capon, D.J.
 Nature 313, 450-458, 1985
 A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus
 A;Reference number: A93355; MUID:8511157; PMID:2982104
 A;Accession: A03974
 A;Molecule type: DNA
 A;Residues: 1-856 <MUE>
 A;Cross-references: GB:R02083; NID:g555008; PIDN:AB59873.1; PID:g328559
 C;Genetics: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
 F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
 F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
 F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 856;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 662 ELDKWA 667

RESULT 23
 VCLJ3W
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
 N;Contains: coat protein gp120; coat protein gp41
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
 C;Accession: A24774
 R;Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
 Cell 45, 637-648, 1986
 A;Title: Identification and characterization of conserved and variable regions in the env
 A;Reference number: A24774; MUID:86218077; PMID:2423250
 A;Accession: A24774
 A;Molecule type: DNA
 A;Residues: 1-856 <STA>
 A;Cross-references: GB:K03455; GB:M38432; NID:g1906382
 C;Genetics: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-29/Domain: signal sequence #status predicted <SIG>
 F;502-847/Product: coat protein gp41 #status predicted <GP1>
 F;87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 100.0%; Score 35; DB 1; Length 856;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 662 ELDKWA 667

RESULT 24
 VCLJWN
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate WN)
 N;Alternate names: coat polyprotein
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
 C;Accession: A28922
 R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Coliatti, E.; Farrell, K.; Wong-Sta
 virology 164, 531-536, 1988
 A;Title: Envelope sequences of two new United States HIV-1 isolates.
 A;Reference number: A28922; MUID:88219542; PMID:3369091
 A;Accession: A28922
 A;Molecule type: DNA
 A;Residues: 1-859 <GUR>
 C;Genetics: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-859/Product: env polyprotein #status predicted <EPP>
 F;87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401

Query Match 100.0%; Score 35; DB 1; Length 859;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 666 ELDKWA 671

RESULT 25
 T01672
 envelope polyprotein precursor - human immunodeficiency virus type 1
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
 C;Accession: T01672
 R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
 Cell 46, 63-74, 1986
 A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol
 A;Reference number: Z14389; MUID:86245056; PMID:2424612
 A;Accession: T01672
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-859 <ALI>
 A;Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28016.1; PID:g60234
 C;Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 859;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 664 ELDKWA 669

RESULT 26

Plant Mol. Biol. 15, 187-190, 1990

A:Title: Nucleotide sequence of a spinach nitrate reductase cDNA.

A:Reference number: S11868; MUID:91355858; PMID:2103436

A:Accession: S11868

A:Molecule type: mRNA

A:Residues: 1-926 <PRO>

A:Cross-references: GB:M32600; NID:g170118; PIDN:AAA34033.1; PID:g170119

R:Shiraishi N.; Kubo, Y.; Takeba, G.; Kiyota, S.; Sakano, K.; Nakagawa, H.

Plant Cell Physiol. 32, 1031-1038, 1991

A:Title: Sequence analysis of cloned cDNA and proteolytic fragments for nitrate reductase

A:Reference number: PQ0694

A:Accession: PQ0694

A:Molecule type: mRNA

A:Residues: 287-926 <SHI>

A:Experimental source: cv. Hoyo

A:Accession: PQ0695

A:Molecule type: protein

A:Residues: 541-550;659-667 <SH2>

R:Quinn, G.B.; Trimboli, A.J.; Prosser, I.M.; Barber, M.J.

Arch. Biochem. Biophys. 327, 151-160, 1996

A:Title: Spectroscopic and kinetic properties of a recombinant form of the flavin domain

A:Reference number: S62777; MUID:96201358; PMID:8615685

A:Accession: S62777

A:Molecule type: protein

A:Residues: 659-673;722-731;758-766;789-798;802-814;829-833;846-852;853-858;859-864;874-879;880-881;882-883;884-885;886-887;888-889;890-891;892-893;894-895;896-897;898-899;900-901;902-903;904-905;906-907;908-909;910-911;912-913;914-915;916-917;918-919;920-921;922-923;924-925;926-927;928-929;930-931;932-933;934-935;936-937;938-939;940-941;942-943;944-945;946-947;948-949;950-951;952-953;954-955;956-957;958-959;960-961;962-963;964-965;966-967;968-969;970-971;972-973;974-975;976-977;978-979;980-981;982-983;984-985;986-987;988-989;990-991;992-993;994-995;996-997;998-999;1000-1001;1002-1003;1004-1005;1006-1007;1008-1009;1010-1011;1012-1013;1014-1015;1016-1017;1018-1019;1020-1021;1022-1023;1024-1025;1026-1027;1028-1029;1030-1031;1032-1033;1034-1035;1036-1037;1038-1039;1040-1041;1042-1043;1044-1045;1046-1047;1048-1049;1050-1051;1052-1053;1054-1055;1056-1057;1058-1059;1060-1061;1062-1063;1064-1065;1066-1067;1068-1069;1070-1071;1072-1073;1074-1075;1076-1077;1078-1079;1080-1081;1082-1083;1084-1085;1086-1087;1088-1089;1090-1091;1092-1093;1094-1095;1096-1097;1098-1099;1100-1101;1102-1103;1104-1105;1106-1107;1108-1109;1110-1111;1112-1113;1114-1115;1116-1117;1118-1119;1120-1121;1122-1123;1124-1125;1126-1127;1128-1129;1130-1131;1132-1133;1134-1135;1136-1137;1138-1139;1140-1141;1142-1143;1144-1145;1146-1147;1148-1149;1150-1151;1152-1153;1154-1155;1156-1157;1158-1159;1160-1161;1162-1163;1164-1165;1166-1167;1168-1169;1170-1171;1172-1173;1174-1175;1176-1177;1178-1179;1180-1181;1182-1183;1184-1185;1186-1187;1188-1189;1190-1191;1192-1193;1194-1195;1196-1197;1198-1199;1200-1201;1202-1203;1204-1205;1206-1207;1208-1209;1210-1211;1212-1213;1214-1215;1216-1217;1218-1219;1220-1221;1222-1223;1224-1225;1226-1227;1228-1229;1230-1231;1232-1233;1234-1235;1236-1237;1238-1239;1240-1241;1242-1243;1244-1245;1246-1247;1248-1249;1250-1251;1252-1253;1254-1255;1256-1257;1258-1259;1260-1261;1262-1263;1264-1265;1266-1267;1268-1269;1270-1271;1272-1273;1274-1275;1276-1277;1278-1279;1280-1281;1282-1283;1284-1285;1286-1287;1288-1289;1290-1291;1292-1293;1294-1295;1296-1297;1298-1299;1300-1301;1302-1303;1304-1305;1306-1307;1308-1309;1310-1311;1312-1313;1314-1315;1316-1317;1318-1319;1320-1321;1322-1323;1324-1325;1326-1327;1328-1329;1330-1331;1332-1333;1334-1335;1336-1337;1338-1339;1340-1341;1342-1343;1344-1345;1346-1347;1348-1349;1350-1351;1352-1353;1354-1355;1356-1357;1358-1359;1360-1361;1362-1363;1364-1365;1366-1367;1368-1369;1370-1371;1372-1373;1374-1375;1376-1377;1378-1379;1380-1381;1382-1383;1384-1385;1386-1387;1388-1389;1390-1391;1392-1393;1394-1395;1396-1397;1398-1399;1400-1401;1402-1403;1404-1405;1406-1407;1408-1409;1410-1411;1412-1413;1414-1415;1416-1417;1418-1419;1420-1421;1422-1423;1424-1425;1426-1427;1428-1429;1430-1431;1432-1433;1434-1435;1436-1437;1438-1439;1440-1441;1442-1443;1444-1445;1446-1447;1448-1449;1450-1451;1452-1453;1454-1455;1456-1457;1458-1459;1460-1461;1462-1463;1464-1465;1466-1467;1468-1469;1470-1471;1472-1473;1474-1475;1476-1477;1478-1479;1480-1481;1482-1483;1484-1485;1486-1487;1488-1489;1490-1491;1492-1493;1494-1495;1496-1497;1498-1499;1500-1501;1502-1503;1504-1505;1506-1507;1508-1509;1510-1511;1512-1513;1514-1515;1516-1517;1518-1519;1520-1521;1522-1523;1524-1525;1526-1527;1528-1529;1530-1531;1532-1533;1534-1535;1536-1537;1538-1539;1540-1541;1542-1543;1544-1545;1546-1547;1548-1549;1550-1551;1552-1553;1554-1555;1556-1557;1558-1559;1560-1561;1562-1563;1564-1565;1566-1567;1568-1569;1570-1571;1572-1573;1574-1575;1576-1577;1578-1579;1580-1581;1582-1583;1584-1585;1586-1587;1588-1589;1590-1591;1592-1593;1594-1595;1596-1597;1598-1599;1600-1601;1602-1603;1604-1605;1606-1607;1608-1609;1610-1611;1612-1613;1614-1615;1616-1617;1618-1619;1620-1621;1622-1623;1624-1625;1626-1627;1628-1629;1630-1631;1632-1633;1634-1635;1636-1637;1638-1639;1640-1641;1642-1643;1644-1645;1646-1647;1648-1649;1650-1651;1652-1653;1654-1655;1656-1657;1658-1659;1660-1661;1662-1663;1664-1665;1666-1667;1668-1669;1670-1671;1672-1673;1674-1675;1676-1677;1678-1679;1680-1681;1682-1683;1684-1685;1686-1687;1688-1689;1690-1691;1692-1693;1694-1695;1696-1697;1698-1699;1700-1701;1702-1703;1704-1705;1706-1707;1708-1709;1710-1711;1712-1713;1714-1715;1716-1717;1718-1719;1720-1721;1722-1723;1724-1725;1726-1727;1728-1729;1730-1731;1732-1733;1734-1735;1736-1737;1738-1739;1740-1741;1742-1743;1744-1745;1746-1747;1748-1749;1750-1751;1752-1753;1754-1755;1756-1757;1758-1759;1760-1761;1762-1763;1764-1765;1766-1767;1768-1769;1770-1771;1772-1773;1774-1775;1776-1777;1778-1779;1780-1781;1782-1783;1784-1785;1786-1787;1788-1789;1790-1791;1792-1793;1794-1795;1796-1797;1798-1799;1800-1801;1802-1803;1804-1805;1806-1807;1808-1809;1810-1811;1812-1813;1814-1815;1816-1817;1818-1819;1820-1821;1822-1823;1824-1825;1826-1827;1828-1829;1830-1831;1832-1833;1834-1835;1836-1837;1838-1839;1840-1841;1842-1843;1844-1845;1846-1847;1848-1849;1850-1851;1852-1853;1854-1855;1856-1857;1858-1859;1860-1861;1862-1863;1864-1865;1866-1867;1868-1869;1870-1871;1872-1873;1874-1875;1876-1877;1878-1879;1880-1881;1882-1883;1884-1885;1886-1887;1888-1889;1890-1891;1892-1893;1894-1895;1896-1897;1898-1899;1900-1901;1902-1903;1904-1905;1906-1907;1908-1909;1910-1911;1912-1913;1914-1915;1916-1917;1918-1919;1920-1921;1922-1923;1924-1925;1926-1927;1928-1929;1930-1931;1932-1933;1934-1935;1936-1937;1938-1939;1940-1941;1942-1943;1944-1945;1946-1947;1948-1949;1950-1951;1952-1953;1954-1955;1956-1957;1958-1959;1960-1961;1962-1963;1964-1965;1966-1967;1968-1969;1970-1971;1972-1973;1974-1975;1976-1977;1978-1979;1980-1981;1982-1983;1984-1985;1986-1987;1988-1989;1990-1991;1992-1993;1994-1995;1996-1997;1998-1999;2000-2001;2002-2003;2004-2005;2006-2007;2008-2009;2010-2011;2012-2013;2014-2015;2016-2017;2018-2019;2020-2021;2022-2023;2024-2025;2026-2027;2028-2029;2030-2031;2032-2033;2034-2035;2036-2037;2038-2039;2040-2041;2042-2043;2044-2045;2046-2047;2048-2049;2050-2051;2052-2053;2054-2055;2056-2057;2058-2059;2060-2061;2062-2063;2064-2065;2066-2067;2068-2069;2070-2071;2072-2073;2074-2075;2076-2077;2078-2079;2080-2081;2082-2083;2084-2085;2086-2087;2088-2089;2090-2091;2092-2093;2094-2095;2096-2097;2098-2099;2100-2101;2102-2103;2104-2105;2106-2107;2108-2109;2110-2111;2112-2113;2114-2115;2116-2117;2118-2119;2120-2121;2122-2123;2124-2125;2126-2127;2128-2129;2130-2131;2132-2133;2134-2135;2136-2137;2138-2139;2140-2141;2142-2143;2144-2145;2146-2147;2148-2149;2150-2151;2152-2153;2154-2155;2156-2157;2158-2159;2160-2161;2162-2163;2164-2165;2166-2167;2168-2169;2170-2171;2172-2173;2174-2175;2176-2177;2178-2179;2180-2181;2182-2183;2184-2185;2186-2187;2188-2189;2190-2191;2192-2193;2194-2195;2196-2197;2198-2199;2200-2201;2202-2203;2204-2205;2206-2207;2208-2209;2210-2211;2212-2213;2214-2215;2216-2217;2218-2219;2220-2221;2222-2223;2224-2225;2226-2227;2228-2229;2230-2231;2232-2233;2234-2235;2236-2237;2238-2239;2240-2241;2242-2243;2244-2245;2246-2247;2248-2249;2250-2251;2252-2253;2254-2255;2256-2257;2258-2259;2260-2261;2262-2263;2264-2265;2266-2267;2268-2269;2270-2271;2272-2273;2274-2275;2276-2277;2278-2279;2280-2281;2282-2283;2284-2285;2286-2287;2288-2289;2290-2291;2292-2293;2294-2295;2296-2297;2298-2299;2300-2301;2302-2303;2304-2305;2306-2307;2308-2309;2310-2311;2312-2313;2314-2315;2316-2317;2318-2319;2320-2321;2322-2323;2324-2325;2326-2327;2328-2329;2330-2331;2332-2333;2334-2335;2336-2337;2338-2339;2340-2341;2342-2343;2344-2345;2346-2347;2348-2349;2350-2351;2352-2353;2354-2355;2356-2357;2358-2359;2360-2361;2362-2363;2364-2365;2366-2367;2368-2369;2370-2371;2372-2373;2374-2375;2376-2377;2378-2379;2380-2381;2382-2383;2384-2385;2386-2387;2388-2389;2390-2391;2392-2393;2394-2395;2396-2397;2398-2399;2400-2401;2402-2403;2404-2405;2406-2407;2408-2409;2410-2411;2412-2413;2414-2415;2416-2417;2418-2419;2420-2421;2422-2423;2424-2425;2426-2427;2428-2429;2430-2431;2432-2433;2434-2435;2436-2437;2438-2439;2440-2441;2442-2443;2444-2445;2446-2447;2448-2449;2450-2451;2452-2453;2454-2455;2456-2457;2458-2459;2460-2461;2462-2463;2464-2465;2466-2467;2468-2469;2470-2471;2472-2473;2474-2475;2476-2477;2478-2479;2480-2481;2482-2483;2484-2485;2486-2487;2488-2489;2490-2491;2492-2493;2494-2495;2496-2497;2498-2499;2500-2501;2502-2503;2504-2505;2506-2507;2508-2509;2510-2511;2512-2513;2514-2515;2516-2517;2518-2519;2520-2521;2522-2523;2524-2525;2526-2527;2528-2529;2530-2531;2532-2533;2534-2535;2536-2537;2538-2539;2540-2541;2542-2543;2544-2545;2546-2547;2548-2549;2550-2551;2552-2553;2554-2555;2556-2557;2558-2559;2560-2561;2562-2563;2564-2565;2566-2567;2568-2569;2570-2571;2572-2573;2574-2575;2576-2577;2578-2579;2580-2581;2582-2583;2584-2585;2586-2587;2588-2589;2590-2591;2592-2593;2594-2595;2596-2597;2598-2599;2600-2601;2602-2603;2604-2605;2606-2607;2608-2609;2610-2611;2612-2613;2614-2615;2616-2617;2618-2619;2620-2621;2622-2623;2624-2625;2626-2627;2628-2629;2630-2631;2632-2633;2634-2635;2636-2637;2638-2639;2640-2641;2642-2643;2644-2645;2646-2647;2648-2649;2650-2651;2652-2653;2654-2655;2656-2657;2658-2659;2660-2661;2662-2663;2664-2665;2666-2667;2668-2669;2670-2671;2672-2673;2674-2675;2676-2677;2678-2679;2680-2681;2682-2683;2684-2685;2686-2687;2688-2689;2690-2691;2692-2693;2694-2695;2696-2697;2698-2699;2700-2701;2702-2703;2704-2705;2706-2707;2708-2709;2710-2711;2712-2713;2714-2715;2716-2717;2718-2719;2720-2721;2722-2723;2724-2725;2726-2727;2728-2729;2730-2731;2732-2733;2734-2735;2736-2737;2738-2739;2740-2741;2742-2743;2744-2745;2746-2747;2748-2749;2750-2751;2752-2753;2754-2755;2756-2757;2758-2759;2760-2761;2762-2763;2764-2765;2766-2767;2768-2769;2770-2771;2772-2773;2774-2775;2776-2777;2778-2779;2780-2781;2782-2783;2784-2785;2786-2787;2788-2789;2790-2791;2792-2793;2794-2795;2796-2797;2798-2799;2800-2801;2802-2803;2804-2805;2806-2807;2808-2809;2810-2811;2812-2813;2814-2815;2816-2817;2818-2819;2820-2821;2822-2823;2824-2825;2826-2827;2828-2829;2830-2831;2832-2833;2834-2835;2836-2837;2838-2839;2840-2841;2842-2843;2844-2845;2846-2847;2848-2849;2850-2851;2852-2853;2854-2855;2856-2857;2858-2859;2860-2861;2862-2863;2864-2865;2866-2867;2868-2869;2870-2871;2872-2873;2874-2875;2876-2877;2878-2879;2880-2881;2882-2883;2884-2885;2886-2887;2888-2889;2890-2891;2892-2893;2894-2895;2896-2897;2898-2899;2900-2901;2902-2903;2904-2905;2906-2907;2908-2909;2910-2911;2912-2913;2914-2915;2916-2917;2918-2919;2920-2921;2922-2923;2924-2925;2926-2927;2928-2929;2930-2931;2932-2933;2934-2935;2936-2937;2938-2939;2940-2941;2942-2943;2944-2945;2946-2947;2948-2949;2950-2951;2952-2953;2954-2955;2956-2957;2958-2959;2960-2961;2962-2963;2964-2965;2966-2967;2968-2969;2970-2971;2972-2973;2974-2975;2976-2977;2978-2979;2980-2981;2982-2983;2984-2985;2986-2987;2988-2989;2990-2991;2992-2993;2994-2995;2996-2997;2998-2999;3000-3001;3002-3003;3004-3005;3006-3007;3008-3009;3010-3011;3012-3013;3014-3015;3016-3017;3018-3019;3020-3021;3022-3023;3024-3025;3026-3027;3028-3029;3030-3031;3032-3033;3034-3035;3036-3037;3038-3039;3040-3041;3042-3043;3044-3045;3046-3047;3048-3049;3050-3051;3052-3053;3054-3055;3056-3057;3058-3059;3060-3061;3062-3063;3064-3065;3066-3067;3068-3069;3070-3071;3072-3073;3074-3075;3076-3077;3078-3079;3080-3081;3082-3083;3084-3085;3086-3087;3088-3089;3090-3091;3092-3093;3094-3095;3096-3097;3098-3099;3100-3101;3102-3103;3104-3105;3106-3107;3108-3109;3110-3111;3112-3113;3114-3115;3116-3117;3118-3119;3120-3121;3122-3123;3124-3125;3126-3127;3128-3129;3130-3131;3132-3133;3134-3135;3136-3137;3138-3139;3140-3141;3142-3143;3144-3145;3146-3147;3148-3149;3150-3151;3152-3153;3154-3155;3156-3157;3158-3159;3160-3161;3162-3163;3164-3165;3166-3167;3168-3169;3170-3171;3172-3173;3174-3175;3176-3177;3178-3179;3180-3181;3182-3183;3184-3185;3186-3187;3188-3189;3190-3191;3192-3193;3194-3195;3196-3197;3198-3199;3200-3201;3202-3203;3204-3205;3206-3207;3208-3209;3210-3211;3212-3213;3214-3215;3216-3217;3218-3219;3220-3221;3222-3223;3224-3225;3226-3227;3228-3229;3230-3231;3232-3233;3234-3235;3

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana chromosome II BAC F4118 genomic sequence.
A:Reference number: 214674
A:Accession: T02448
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-268 <ROU>
A:Cross-references: EMBL:AC004665; NID:g3386593; PID:g3386596
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.V.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Unayam, L.; Tallon, J.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.B.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: D84897
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <STO>
A:Cross-references: GB:AR002093; NID:g3702346; PIDN:AAC62903.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g45990; F4118.3
A:Map position: 2
A:Introns: 267/3; 53/3; 83/3; 139/2; 162/3; 189/2; 210/2; 236/1
Query Match 91.4%; Score 32; DB 2; Length 268;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 227 ELDKWS 232
RESULT 30
E71561
probable solute protein binding - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 17-Mar-2000
C:Accession: E71561
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marache, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: E71561
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-326 <ARN>
A:Cross-references: GB:AR001281; GB:AR001273; NID:g3328454; PIDN:AAC67658.1; PID:g332846
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: YtgA
C:Superfamily: adhesin B
Query Match 91.4%; Score 32; DB 2; Length 326;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 184 ELDRWA 189
RESULT 31
D71274
probable prolipoprotein diacylglycerol transferase (lgt) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 15-Sep-2000
C:Accession: D71274
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uitterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: D71274
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-332 <COL>
A:Cross-references: GB:AE001255; GB:AE000520; NID:g3323156; PIDN:AAC65817.1; PID:g332316
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0852
C:Superfamily: prolipoprotein diacylglycerol transferase
Query Match 91.4%; Score 32; DB 2; Length 332;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 47 ELDKWS 52
RESULT 32
C83347
probable dipeptidase precursor PA2393 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83347
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C83347
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-448 <STO>
A:Cross-references: GB:AE004665; GB:AE004091; NID:g9948426; PIDN:AAG05781.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2393
Query Match 91.4%; Score 32; DB 2; Length 448;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 180 QLDKWA 185
RESULT 33
S51160
nitrate reductase (NADH) (EC 1.7.1.1) (clone Zmr1S) - maize (fragment)
C:Species: Zea mays (maize)
C:Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 03-Jun-2002
C:Accession: S51160
R:Campbell, W.H.
submitted to the EMBL Data Library, May 1994
A:Description: Expression in Escherichia coli of cytochrome c reductase activity from a
A:Reference number: S51160
A:Accession: S51160
A:Molecule type: mRNA
A:Residues: 1-501 <CAM>
A:Cross-references: EMBL:M77792; NID:g168516; PIDN:AAA33483.1; PID:g168517
A:Experimental source: strain W64xW182E; scutellum
C:Genetics:
A:Gene: nar-1S
C:Complex: homodimer
C:Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 redu
C:Keywords: dimer; electron transfer; FAD; flavoprotein; heme; iron; metalloprotein; mol
F;1-67/Domain: molybdopterin-binding domain homology (fragment) <PCO>

F;129-203/Domain: cytochrome b5 core homology <CB5>
F;248-501/Domain: cytochrome-b5 reductase homology <CBR>
F;164,187/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 91.4%; Score 32; DB 2; Length 501;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 417 ELDRWA 422
|||||

RESULT 34
S19254
nitrate reductase (NADH) (EC 1.7.1.1) flavin chain (clone Zmnr1) - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 03-Jun-2002
C;Accession: S19254; S58710; A35499
R;Gowri, G.; Campbell, W.H., 1989
Plant Physiol. 90, 792-798, 1989
A;Title: cDNA clones for corn leaf NADH: nitrate reductase and chloroplast NAD(P) (+): gl
A;Reference number: S19254
A;Accession: S19254
A;Molecule type: mRNA
A;Residues: 1-617 <GOW>
A;Cross-references: EMBL:M27821
A;Accession: S58710
A;Molecule type: protein
A;Residues: 'RII', '369', 'TPA', '373', 'SDNYHFKEIAVRWD', '390', 'S', '392', 'NTHLETAIAAPG', '406', 'K', '4
R;Hyde, G.E.; Campbell, W.H.
Biochem. Biophys. Res. Commun. 168, 1285-1291, 1990
A;Title: High-level expression in Escherichia coli of the catalytically active flavin do
A;Reference number: A35499; MUID:90267474; PMID:2189408
A;Accession: A35499
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 364-388, 'DQ', '391-404', 'SI', '407-413', 'AV', '415', 'P', '417-617 <HYD>
A;Cross-references: GB:M27821
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 red
C;Keywords: dimer; electron transfer; FAD; flavoprotein; heme; iron; metalloprotein; mol
F;1-187/Domain: molybdopter-in-binding domain homology (fragment) <PCO>
F;1249-323/Domain: cytochrome b5 core homology <CB5>
F;368-617/Domain: cytochrome-b5 reductase homology <CBR>
F;284,307/Binding site: heme iron (His) (axial ligands) #status predicted
F;431,589/Binding site: NAD (Lys, Cys) #status predicted
F;471/Binding site: FAD (Tyr) #status predicted

Query Match 91.4%; Score 32; DB 2; Length 617;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 536 ELDRWA 541
|||||

RESULT 35
VCLJH4
env polypeptide - human immunodeficiency virus type 1 (isolate CDC-451)
N;Alternate names: coat polypeptide
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1 HIV-1
C;Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: C25523
R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare,
Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human
A;Reference number: A94136; MUID:87041461; PMID:3490666
A;Accession: C25523
A;Molecule type: DNA
A;Residues: 1-868 <DES>
A;Cross-references: GB:M13137; NID:G326460; PIDN:AAA44311.1; PID:G326467

C;Genetics:
A;Superfamily: type E retrovirus env polypeptide
C;Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane protei
F;1-521/Product: coat protein gp120 #status predicted <GP1>
F;522-868/Product: coat protein gp41 #status predicted <GP2>
F;89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459,
Query Match 91.4%; Score 32; DB 1; Length 868;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 674 QLDKWA 679
|||||

RESULT 36
T02240
nitrate reductase [NAD(P)H] (EC 1.7.1.2) - maize
C;Species: Zea mays (maize)
C;Date: 05-Mar-1999 #sequence revision 05-Mar-1999 #text_change 03-Jun-2002
C;Accession: T02240
R;Campbell, W.H.; Redinbaugh, M.G.; Ingemarsson, B.; Dougherty, E.S.; Campbell, E.R.
submitted to the EMBL Data Library, January 1995
A;Description: A third nitrate reductase gene is expressed in corn tissues and suspensio
A;Reference number: Z14635
A;Accession: T02240
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-889 <CAM>
A;Cross-references: EMBL:U20450; NID:G676849; PIDN:AAA62316.1; PID:G676850
A;Experimental source: strain B73; seedling
C;Genetics:
A;Introns: 336/1; 383/1; 460/3
C;Function:
A;Description: catalyzes the reduction of nitrate to nitrite using NAD(P)H as the electr
A;Pathway: nitrate assimilation
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 red
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; molybdenum; mol
F;82-469/Domain: molybdopter-in-binding domain homology <PCO>
F;520-594/Domain: cytochrome b5 core homology <CB5>
F;637-889/Domain: cytochrome-b5 reductase homology <CBR>
F;181/Binding site: molybdopter-in (Cys) (covalent) #status predicted
F;420/Disulfide bonds: interchain #status predicted
F;555,578/Binding site: heme iron (His) (axial ligands) #status predicted
F;701,861/Binding site: NAD(P) (Lys, Cys) #status predicted
F;741/Binding site: FAD (Tyr) #status predicted

Query Match 91.4%; Score 32; DB 2; Length 889;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 806 ELDRWA 811
|||||

RESULT 37
RDBHNS
nitrate reductase (NADH) (EC 1.7.1.1) - barley (cv. Steptoe) (fragment)
C;Species: Hordeum vulgare (barley)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 03-Jun-2002
C;Accession: S17454
R;Schnorr, K.M.; Juricek, M.; Huang, C.; Culley, D.; Kleinhofs, A.
Mol. Gen. Genet. 227, 411-416, 1991
A;Title: Analysis of barley nitrate reductase cDNA and genomic clones.
A;Reference number: S17453; MUID:91326031; PMID:1865878
A;Accession: S17454
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-912 <SCH>
A;Cross-references: EMBL:X57844; NID:g19044; PIDN:CAA40975.1; PID:g19045

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1991
 C;Genetics:
 A;Map position: 6
 C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
 C;Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
 F;82-474/Domain: molybdopterin-binding domain homology <PCO>
 F;535-609/Domain: cytochrome b5 core homology <CB5>
 F;658-912/Domain: cytochrome-b5 reductase homology <CBR>
 F;186/Binding site: molybdopterin (Cys) (covalent) #status predicted
 F;425/Disulfide bonds: interchain #status predicted
 F;570,593/Binding site: heme iron (His) (axial ligands) #status predicted
 F;722,884/Binding site: NAD (Lys, Cys) #status predicted
 F;763/Binding site: FAD (Tyr) #status predicted

Query Match 91.4%; Score 32; DB 1; Length 912;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||:|
 Db 828 ELDRWA 833

RESULT 38
 RDBNH
 nitrate reductase (NADH) (EC 1.7.1.1) - barley (cv. Himalaya)
 C;Species: Hordeum vulgare (barley)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Jun-2002
 C;Accession: S17453
 R;Schnorr, K.M.; Juricek, M.; Huang, C.; Culley, D.; Kleinhofs, A.
 Mol. Gen. Genet. 227, 411-416, 1991
 A;Title: Analysis of barley nitrate reductase cDNA and genomic clones.
 A;Reference number: S17453; MUID:91326031; PMID:1865878
 A;Accession: S17453
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-915 <SCH>
 A;Cross-references: EMBL:X57845; NID:gl8993; PIDN:CAA40976.1; PID:gl8994
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1991
 C;Genetics:
 A;Map position: 6
 A;Introns: 391/1
 C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
 C;Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
 F;85-477/Domain: molybdopterin-binding domain homology <PCO>
 F;538-612/Domain: cytochrome b5 core homology <CB5>
 F;661-915/Domain: cytochrome-b5 reductase homology <CBR>
 F;189/Binding site: molybdopterin (Cys) (covalent) #status predicted
 F;428/Disulfide bonds: interchain #status predicted
 F;573,596/Binding site: heme iron (His) (axial ligands) #status predicted
 F;725,887/Binding site: NAD (Lys, Cys) #status predicted
 F;766/Binding site: FAD (Tyr) #status predicted

Query Match 91.4%; Score 32; DB 1; Length 915;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||:|
 Db 831 ELDRWA 836

RESULT 39
 S07554
 nitrate reductase (NADH) (EC 1.7.1.1) - rice
 C;Species: Oryza sativa (rice)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Jun-2002
 C;Accession: S07554
 R;Choi, H.K.; Kleinhofs, A.; An, G.
 Plant Mol. Biol. 13, 731-733, 1989
 A;Title: Nucleotide sequence of rice nitrate reductase genes.
 A;Reference number: S07554; MUID:91370859; PMID:2491689
 A;Accession: S07554

A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-916 <CHO>
 A;Cross-references: EMBL:X15819
 C;Genetics:
 A;Gene: nial
 A;Introns: 347/1; 394/1; 471/3
 C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
 C;Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
 F;88-480/Domain: molybdopterin-binding domain homology <PCO>
 F;541-615/Domain: cytochrome b5 core homology <CB5>
 F;663-916/Domain: cytochrome-b5 reductase homology <CBR>
 F;192/Binding site: molybdopterin (Cys) (covalent) #status predicted
 F;431/Disulfide bonds: interchain #status predicted
 F;576,599/Binding site: heme iron (His) (axial ligands) #status predicted
 F;727,888/Binding site: NAD(P) (Lys, Cys) #status predicted
 F;767/Binding site: FAD (Tyr) #status predicted

Query Match 91.4%; Score 32; DB 2; Length 916;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||:|
 Db 832 ELDRWA 837

RESULT 40
 S77910
 hypothetical protein 1 - grapevine virus A
 C;Species: Grapevine virus A
 C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
 C;Accession: S77910
 R;Minafra, A.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: S77910
 A;Accession: S77910
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1707 <MIN>
 A;Cross-references: EMBL:X75433; NID:gl405614; PIDN:CAA53182.1; PID:gl405615
 C;Superfamily: grapevine trichovirus B hypothetical protein

Query Match 91.4%; Score 32; DB 2; Length 1707;
 Best Local Similarity 83.3%; Pred. No. 4.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||:|
 Db 1457 DLDKWA 1462

RESULT 41
 E82798
 hypothetical protein XF0509 [imported] - Xylella fastidiosa (strain 9a5c)
 C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C;Accession: E82798
 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below

A;Accession: E82798
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-78 <SIM>
 A;Cross-references: GB:AE003899; GB:AE003849; NID:99105351; PIDN:AAF83319.1; GSPDB:GN001
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dorfy, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to Genbank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; France, S.C.; Franco, M.C.; Fromm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A;Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tshakho, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

Query Match 88.6%; Score 31; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
|||||
Db 42 ELDKW 46

RESULT 42
C64746
yafu protein - Escherichia coli (strain K-12)
N;Alternate names: hypothetical protein b0218
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: C64746
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64746
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-112 <BLAT>
A;Cross-references: GB:AE000130; GB:U00096; NID:g1786402; PIDN:AACT3322.1; PID:g1786411;
A;Experimental source: strain K-12, substrain MGI655
C;Genetics:
A;Gene: yafu
C;Superfamily: Escherichia coli yafu protein

Query Match 88.6%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
|||||
Db 90 ELDKW 94

RESULT 43
H70387
hypothetical protein aq_1018 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jun-2000
C;Accession: H70387
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196866; PMID:9537320
A;Accession: H70387
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-126 <AQF>
A;Cross-references: GB:AE000718; NID:G2983504; PIDN:AACT07091.1; PID:G2983514; GB:AE00069
A;Experimental source: strain VFS
C;Genetics:
A;Gene: aq_1018
C;Superfamily: Aquifex aeolicus hypothetical protein aq_1018

Query Match 88.6%; Score 31; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
|||||
Db 95 ELDKW 99

RESULT 44
AB0550
conserved hypothetical protein STY0420 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0550
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0550
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08842.1; PID:g16501656; GSPDB:GN00176
C;Genetics:
A;Gene: STY0420
C;Superfamily: yaiI protein

Query Match 88.6%; Score 31; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
|||||
Db 139 ELDKW 143

RESULT 45
AH0368
conserved hypothetical protein YPO3033 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AH0368
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB00001; MUID:21470413; PMID:11586360
A;Accession: AH0368
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <YPO>
A;Cross-references: GB:AL590842; PIDN:CAC92275.1; PID:g15980986; GSPDB:GN00175
C;Genetics:
A;Gene: YPO3033
C;Superfamily: yaiI protein

Query Match 88.6%; Score 31; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
|||||
Db 139 ELDKW 143

RESULT 46

A45332
zipper protein - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C:Accession: A45332
R:Bikle, D.D.; Munson, S.; Morrison, N.; Eisman, J.
J. Biol. Chem. 268, 620-626, 1993
A:Title: Zipper protein, a newly described tropomyosin-like protein of the intestinal brush border.
A:Reference number: A45332; MUID:93107070; PMID:7678004
A:Accession: A45332
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-201 <BIK>
A:Experimental source: intestine
A>Note: sequence extracted from NCBI backbone (NCBIP:121450)

Query Match 88.6%; Score 31; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKW 5
|||||
Db 62 ELDKW 66

RESULT 47
AF1167
ABC transporter, ATP-binding protein homolog lmo0742 [imported] - Listeria monocytogenes
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AF1167
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1167
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-229 <GLA>
A:Cross-references: GB:NC 003210; PIDN:CAC98920.1; PID:g16410131; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0742

Query Match 88.6%; Score 31; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKW 5
|||||
Db 104 ELDKW 108

RESULT 48
B83030
probable rRNA methylase PA4936 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83030
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: B83030
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <STO>

A:Cross-references: GB:AE004906; GB:AE004091; NID:99951206; PIDN:AAG08321.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4936
C:Superfamily: conserved hypothetical protein HI0860

Query Match 88.6%; Score 31; DB 2; Length 248;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 59 ELDEWA 64

RESULT 49
T33683
hypothetical protein T12B5.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
C:Accession: T33683
R:Langston, Y.; Wohldmann, P.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of C. elegans cosmid T12B5.
A:Reference number: Z21387
A:Accession: T33683
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-338 <LAN>
A:Cross-references: EMBL:AF100307; PIDN:AAC68928.1; GSPDB:GN000021; CESP:T12B5.2
A:Experimental source: strain Bristol N2; clone T12B5
C:Genetics:
A:Gene: CESP:T12B5.2
A:Map position: 3
A:Introns: 34/2; 62/2; 269/3
C:Superfamily: Caenorhabditis elegans hypothetical protein ZC47.9

Query Match 88.6%; Score 31; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKW 5
|||||
Db 19 ELDKW 23

RESULT 50
T20280
hypothetical protein cTel54X.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
C:Accession: T20280
R:Smay, R.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z19248
A:Accession: T20280
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-343 <WIL>
A:Cross-references: EMBL:AL031226; PIDN:CAA20224.1; GSPDB:GN000021; CESP:cTel54X.1
C:Genetics:
A:Gene: CESP:cTel54X.1
A:Map position: 3
A:Introns: 34/2; 62/2; 265/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C29F9.11

Query Match 88.6%; Score 31; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKW 5
|||||
Db 19 ELDKW 23

Search completed: March 16, 2004, 09:18:20
Job time : 31 secs



GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2004, 09:09:50 ; Search time 11 Seconds
(without alignments)
28.402 Million cell updates/sec

Title: US-10-024-329-2

Perfect score: 35

Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	464	1 KYNV_RAT	P70712 rattus norv
2	35	100.0	465	1 KYNV_HUMAN	Q16719 homo sapien
3	35	100.0	817	1 YR86_CABEL	Q09568 caenorhabdi
4	35	100.0	846	1 ENV_HV1ND	P18799 human immun
5	35	100.0	847	1 ENV_HV1S1	P19550 human immun
6	35	100.0	847	1 ENV_HV1W2	P05880 human immun
7	35	100.0	848	1 ENV_HV1JR	P20871 human immun
8	35	100.0	851	1 ENV_HV1B8	P04582 human immun
9	35	100.0	852	1 ENV_HV1BN	P12488 human immun
10	35	100.0	852	1 ENV_HV1S3	P19549 human immun
11	35	100.0	853	1 ENV_HV1EL	P04581 human immun
12	35	100.0	853	1 ENV_HV1MF	P19551 human immun
13	35	100.0	853	1 ENV_HV1F2	P12487 human immun
14	35	100.0	855	1 ENV_HV1A2	P03378 human immun
15	35	100.0	855	1 ENV_HV1OY	P04580 human immun
16	35	100.0	855	1 ENV_HV1Z6	P04580 human immun
17	35	100.0	856	1 ENV_HV1B1	P04581 human immun
18	35	100.0	856	1 ENV_HV1H2	P04578 human immun
19	35	100.0	856	1 ENV_HV1H3	P04624 human immun
20	35	100.0	856	1 ENV_HV1LW	Q70626 human immun
21	35	100.0	856	1 ENV_HV1MN	P05877 human immun
22	35	100.0	856	1 ENV_HV1PV	P03376 human immun
23	35	100.0	856	1 ENV_HV1SC	P05878 human immun
24	35	100.0	856	1 ENV_HV1W1	P11872 human immun
25	35	100.0	859	1 ENV_HV1MA	P04583 human immun
26	35	100.0	861	1 ENV_HV1BR	P03377 human immun
27	35	100.0	865	1 ENV_HV1RH	P04579 human immun
28	35	100.0	926	1 NIA_SPIOL	P23312 spinacia ol
29	32	91.4	326	1 Y067_CHLTP	Q98529 chlamydia t
30	32	91.4	332	1 LGT_TREP	O83824 treponema p
31	32	91.4	358	1 T2SL_STRAH	Q31074 streptomyce
32	32	91.4	621	1 NIA1_MAIZE	P17571 zea mays (m
33	32	91.4	863	1 ENV_HV1Z8	P05882 human immun

34	32	91.4	868	1 ENV_HV1C4	P05879 human immun
35	32	91.4	889	1 NIA3_MAIZE	P49102 zea mays (m
36	32	91.4	912	1 NIA2_HORVU	P27969 hordeum vul
37	32	91.4	915	1 NIA1_HORVU	P27967 hordeum vul
38	32	91.4	916	1 NIA1_ORYSA	P16081 oryza sativ
39	32	91.4	1073	1 ACA9_ARATH	Q91441 arabidopsis
40	31	88.6	112	1 YAFU_ECOLI	P77354 escherichia
41	31	88.6	151	1 YAI1_SALTY	Q8xemi salmonella
42	31	88.6	152	1 YU33_YERPE	Q8zcf8 yersinia pe
43	31	88.6	381	1 DHB2_MOUSE	P51658 mus musculu
44	31	88.6	388	1 GAG_HV1W2	P05889 human immun
45	31	88.6	392	1 GAL1_STRPN	Q97nz6 streptococ
46	31	88.6	392	1 GAL1_STRR6	Q8dnk7 streptococ
47	31	88.6	421	1 ECB2_HALEL	O52250 halomonas e
48	31	88.6	498	1 GAG_HV1OY	P20889 human immun
49	31	88.6	499	1 GAG_HV1N5	P12493 human immun
50	31	88.6	499	1 GAG_HV1Y2	P35962 human immun
51	31	88.6	501	1 GAG_HV1A2	P03349 human immun
52	31	88.6	785	1 APE3_SULSO	P05928 sulfolobus
53	31	88.6	854	1 ENV_SIVCZ	P17281 chimpanzee
54	31	88.6	880	1 SYV_BACST	P11931 bacillus st
55	31	88.6	881	1 NIA1_PHAVU	P39865 phaseolus v
56	31	88.6	886	1 NIA1_SOYBN	P54233 glycine max
57	31	88.6	890	1 NIA2_SOYBN	P39870 glycine max
58	31	88.6	1050	1 LKTA_ACTAC	P16462 actinobacil
59	31	88.6	1235	1 VGL2_CVMJH	P11225 murine coro
60	31	88.6	1324	1 VGL2_CVMA5	P11224 murine coro
61	31	88.6	1376	1 VGL2_CVM4	P22432 murine coro
62	31	88.6	1376	1 VGL2_CVMJC	Q02385 murine coro
63	31	88.6	1586	1 SN22_HUMAN	P51531 homo sapien
64	31	88.6	1647	1 SN24_HUMAN	P51532 homo sapien
65	30	85.7	478	1 KYNV_CABEL	Q18026 caenorhabdi
66	30	85.7	568	1 FLP_ZYGB1	P13784 zygoacchar
67	30	85.7	612	1 PEX5_YEAST	P35056 saccharomyc
68	30	85.7	722	1 GUNF_CLOCE	P37698 clostridium
69	30	85.7	843	1 ENV_HV1Y2	P35961 human immun
70	30	85.7	856	1 ENV_HV1Z8	P05881 human immun
71	30	85.7	867	1 ENV_HV1J3	P12489 human immun
72	30	85.7	891	1 NIA7_HORVU	P27968 hordeum vul
73	30	85.7	897	1 SYI_FERPE	Q9kdb4 ferdobact
74	30	85.7	904	1 NIA1_TOBAC	P11605 nicotiana t
75	30	85.7	904	1 NIA2_TOBAC	P08509 nicotiana t
76	30	85.7	909	1 NIA_FETHY	P36859 petunia hyb
77	30	85.7	939	1 SYI_BUCBP	Q89au9 buchnera ap
78	30	85.7	940	1 SYI_BUCAI	P57249 buchnera ap
79	30	85.7	2507	1 NBEA_CABEL	Q19317 caenorhabdi
80	30	85.7	4910	1 MDN1_YEAST	Q12019 saccharomyc
81	29	82.9	129	1 RS1A_DICDI	P46793 dictyosteli
82	29	82.9	160	1 NIA_LOTTE	P39882 lotus tetra
83	29	82.9	255	1 RECO_LISMO	Q8y752 listeria mo
84	29	82.9	283	1 RPCI_BPP1	P13121 bacterioph
85	29	82.9	283	1 RPCI_BPP7	P13122 bacterioph
86	29	82.9	326	1 Y338_CHLPM	Q9pkx2 chlamydia m
87	29	82.9	401	1 ASSY_XYLFA	Q9pem9 xyella fas
88	29	82.9	445	1 MESJ_XYLFT	P59606 xyella fas
89	29	82.9	445	1 MESJ_XYLFT	Q8ka23 buchnera ap
90	29	82.9	494	1 COAT_CERV	P05399 carnation e
91	29	82.9	531	1 NKFF3_HUMAN	Q9h4d5 homo sapien
92	29	82.9	565	1 CN1A_MOUSE	Q61481 mus musculu
93	29	82.9	623	1 BKLJ_HUMAN	Q81y47 homo sapien
94	29	82.9	630	1 SYR_PYRAE	Q8zta8 pyrobaculum
95	29	82.9	808	1 PDAL_TOBAC	P93400 nicotiana t
96	29	82.9	809	1 PDAL_VIGUN	O04865 vigna ungui
97	29	82.9	812	1 PDAL_MAIZE	Q43270 zea mays (m
98	29	82.9	890	1 NIA2_PHAVU	P39866 phaseolus v
99	29	82.9	898	1 NIA_BETVR	P27783 betula verr
100	29	82.9	900	1 NIA_LOTJA	P39869 lotus japon
101	29	82.9	911	1 NIA_LYCES	P17570 lycopersico
102	29	82.9	918	1 NIA_CUCNA	P17569 cucurbita m
103	29	82.9	920	1 NIA_CICIN	P43101 cichorium i
104	29	82.9	1132	1 VHSJ_LAMBD	P03749 bacterioph
105	29	82.9	1337	1 YDM5_SCHPO	P87136 schizosacch
106	28	80.0	109	1 PHS_VIBCH	Q9klb9 vibrio chol

107	28	80.0	140	1	LYSS DROME	P37160 drosophila	180	27	77.1	292	1	Y240_MYCGE	P47482 mycoplasma
108	28	80.0	155	1	Y4A4_PSEAE	Q9hx23 pseudomonas	181	27	77.1	306	1	MNTA_BACSU	Q34385 bacillus su
109	28	80.0	155	1	YCC6_PSEPK	Q8d17 pseudomonas	182	27	77.1	309	1	P2AA_CHICK	P48463 gallus gall
110	28	80.0	155	1	YCC6_PSEPK	Q8d17 pseudomonas	183	27	77.1	309	1	P2AA_HUMAN	P05323 homo sapien
111	28	80.0	173	1	NUDH_RHTLO	Q98f04 rhizobium l	184	27	77.1	309	1	P2AA_MOUSE	P13353 mus musculu
112	28	80.0	191	1	NADD_STAEP	Q8cscl staphylococ	185	27	77.1	309	1	P2AB_HUMAN	P11082 homo sapien
113	28	80.0	194	1	HAM2_BACHD	Q9k8d9 bacillus ha	186	27	77.1	309	1	P2AB_RABIT	P11611 oryctolagus
114	28	80.0	195	1	OBL_OBELO	Q27709 obelia long	187	27	77.1	320	1	CCSA_MARPO	P12214 marchantia
115	28	80.0	200	1	ENGB_CLOAB	Q37fu0 clostridium	188	27	77.1	324	1	Y518_CHLPC	Q9z834 chlamydia p
116	28	80.0	200	1	NADD_CLOAB	Q57fj12 clostridium	189	27	77.1	335	1	TRD2_SPCO	Q9z4w9 streptomyce
117	28	80.0	281	1	MODD_HAEIN	Q57278 haemophilus	190	27	77.1	348	1	YLM1_CABEL	P34404 caenorhabdi
118	28	80.0	283	1	Y97_CABEL	Q09245 caenorhabdi	191	27	77.1	381	1	YJ04_SCHPO	P44045 schizosacch
119	28	80.0	327	1	CI30_HUMAN	Q9y375 homo sapien	192	27	77.1	382	1	DXR_CHLTE	Q8kg43 chlorobium
120	28	80.0	328	1	CI30_MOUSE	Q9cwx2 mus musculu	193	27	77.1	390	1	ADHB_CLOAB	Q44953 clostridium
121	28	80.0	339	1	YNZ8_CABEL	P45968 caenorhabdi	194	27	77.1	400	1	DFP_HAEIN	P44953 haemophilus
122	28	80.0	348	1	LLY_LEGPN	Q53407 legionella	195	27	77.1	404	1	DXR_PROMP	Q7v0w0 prochloroco
123	28	80.0	370	1	RECF_BACSU	P05651 bacillus su	196	27	77.1	406	1	CAIB_PROSL	Q8gb19 proteus sp.
124	28	80.0	372	1	REP2_SYNG3	P74476 synchocyst	197	27	77.1	409	1	Y148_MYCGE	P47394 mycoplasma
125	28	80.0	374	1	RECF_LACPL	Q890k5 lactobacill	198	27	77.1	437	1	NEOR_STRCY	P14501 streptomyce
126	28	80.0	377	1	MTC3_CHVNL	P10835 chlorella v	199	27	77.1	445	1	Y148_MYCPN	P75584 mycoplasma
127	28	80.0	379	1	YN30_MYCTU	Q10514 mycobacteri	200	27	77.1	487	1	C135_DROME	Q9vgb5 drosophila
128	28	80.0	406	1	DFP_ECOLI	P24285 escherichia	201	27	77.1	499	1	GAG_HVIEL	P04592 human immun
129	28	80.0	445	1	DHE2_PORGI	Q03578 porphyromon	202	27	77.1	500	1	GAG_HVIRH	P05890 human immun
130	28	80.0	457	1	CFXA_ECOLI	P08336 escherichia	203	27	77.1	514	1	CP24_HUMAN	Q07973 homo sapien
131	28	80.0	499	1	GAG_HV1CA	P05887 human immun	204	27	77.1	514	1	CP24_MOUSE	Q64441 mus musculu
132	28	80.0	499	1	GAG_HV1H2	P04591 human immun	205	27	77.1	522	1	CP24_RAT	Q09128 rattus norv
133	28	80.0	499	1	GAG_HV1J3	P12494 human immun	206	27	77.1	522	1	CP24_HUMAN	Q8n9f8 homo sapien
134	28	80.0	503	1	GAG_HV1J3	P20873 human immun	207	27	77.1	532	1	IP47_SHIFL	P18014 shigella fl
135	28	80.0	506	1	GAG_HV1WN	P05888 human immun	208	27	77.1	537	1	IPYR_RICCN	Q92197 rickettsia
136	28	80.0	511	1	GAG_HV1B1	P03347 human immun	209	27	77.1	556	1	BETA_ECOLI	P17444 escherichia
137	28	80.0	511	1	GAG_HV1B5	P04593 human immun	210	27	77.1	560	1	YF31_SCHPO	Q10684 schizosacch
138	28	80.0	511	1	GAG_HV1B8	P03348 human immun	211	27	77.1	565	1	MAOX_SCHPO	P40375 schizosacch
139	28	80.0	511	1	GAG_HV1PV	P03350 human immun	212	27	77.1	571	1	YK18_YEAST	P18009 shigella fl
140	28	80.0	533	1	UBIB_PSEAE	Q9hub8 pseudomonas	213	27	77.1	574	1	IPA4_SHIFL	P19813 oryctolagus
141	28	80.0	620	1	SMP_COTJA	Q2154 coturnix co	214	27	77.1	578	1	TREA_RABIT	P19813 oryctolagus
142	28	80.0	623	1	YD54_MYCTU	Q11024 mycobacteri	215	27	77.1	586	1	PYRG_RICPR	Q9zdf1 rickettsia
143	28	80.0	650	1	TDR3_MOUSE	Q91w18 mus musculu	216	27	77.1	587	1	GOX_PENAG	P81156 penicillium
144	28	80.0	725	1	MAZ2_PSESM	Q87z72 pseudomonas	217	27	77.1	596	1	TREA_DROME	Q9w2m2 drosophila
145	28	80.0	808	1	PAI1_FIMBR	Q40883 pampinella	218	27	77.1	605	1	GOX_TALFL	Q9w2m2 drosophila
146	28	80.0	956	1	NIA2_ARATH	P10335 arabidopsis	219	27	77.1	623	1	ASH2_MOUSE	Q91x20 mus musculu
147	28	80.0	956	1	SVY_TREPA	Q83998 treponema p	220	27	77.1	628	1	ASH2_HUMAN	Q9ub13 homo sapien
148	28	80.0	1004	1	LV10_MOUSE	P23249 mus musculu	221	27	77.1	628	1	YKPS_YEAST	P36056 saccharomyc
149	28	80.0	1227	1	LAF4_HUMAN	P18126 homo sapien	222	27	77.1	639	1	YGFT_ECOLI	Q08979 saccharomyc
150	28	80.0	1272	1	FWR2_MOUSE	O55112 mus musculu	223	27	77.1	651	1	KEL3_YEAST	P60285 homo sapien
151	28	80.0	1297	1	SOS2_MOUSE	Q02384 mus musculu	224	27	77.1	661	1	ARKS_HUMAN	Q9y7x6 schizosacch
152	28	80.0	1311	1	FMR2_HUMAN	P51816 homo sapien	225	27	77.1	684	1	ISH1_SCHPO	Q27483 caenorhabdi
153	28	80.0	1319	1	SOS1_MOUSE	Q62245 mus musculu	226	27	77.1	756	1	K6PF_CABEL	P83436 homo sapien
154	28	80.0	1323	1	RRPO_SMYEA	P28897 strawberry	227	27	77.1	770	1	COG7_HUMAN	Q9cfh4 lactococcus
155	28	80.0	1332	1	SOS2_HUMAN	Q07890 homo sapien	228	27	77.1	843	1	PIWI_DROME	Q9vkm1 drosophila
156	28	80.0	1333	1	SOS1_HUMAN	Q07889 homo sapien	229	27	77.1	851	1	MUTS_YERPE	Q8zbq3 yersinia pe
157	28	80.0	1430	1	PPPU_HUMAN	Q92729 homo sapien	230	27	77.1	853	1	MUTS_ECO57	Q986p8 escherichia
158	28	80.0	2145	1	US20_CABEL	Q9u290 caenorhabdi	231	27	77.1	853	1	MUTS_ECOLI	Q8fel3 escherichia
159	28	80.0	2363	1	SPCO_MOUSE	Q62261 mus musculu	232	27	77.1	853	1	MUTS_ECOLI	P23199 escherichia
160	28	80.0	3264	1	SPCO_HUMAN	Q01082 homo sapien	233	27	77.1	855	1	MUTS_VIBPA	Q81339 salmonella
161	28	80.0	3712	1	ACVS_CEPAC	P25464 cephalospor	234	27	77.1	860	1	MUTS_PASMU	P57972 pasteurella
162	28	77.1	64	1	VRAL_BBP22	P14113 bacterioph	235	27	77.1	861	1	MUTS_HARIN	P44834 haemophilus
163	27	77.1	66	1	VRAL_LAMB2	P03703 bacterioph	236	27	77.1	862	1	MUTS_VIRCH	Q9kub2 vibrio chol
164	27	77.1	76	1	VRAL_BPPH3	P07235 bacterioph	237	27	77.1	876	1	SYL_AGR75	Q8ubv2 agrobacteri
165	27	77.1	100	1	Y939_AERPE	Q9ydh4 aeropyrum p	238	27	77.1	916	1	SCRB_LIMPO	Q25386 limulus pol
166	27	77.1	103	1	RS10_CHLTE	Q8kahl chlorobium	239	27	77.1	917	1	CP3_DROME	Q9xyp8 drosophila
167	27	77.1	151	1	YAI1_ECOLI	Q9nlp6 drosophila	240	27	77.1	925	1	PDC2_YEAST	P32896 saccharomyc
168	27	77.1	152	1	E1BS_ADEL2	P52088 escherichia	241	27	77.1	937	1	SVI_ECOLI	P00956 escherichia
169	27	77.1	163	1	RS6_MYCGE	P04492 human adeno	242	27	77.1	938	1	SVI_ECOLI	Q8k922 buchnera ap
170	27	77.1	208	1	NADD_BUCAL	P47336 mycoplasma	243	27	77.1	941	1	SVI_HAEIN	P43824 haemophilus
171	27	77.1	214	1	NADD_BUCAL	P57521 buchnera ap	244	27	77.1	941	1	SVI_HAEIN	P43824 haemophilus
172	27	77.1	243	1	CLCA_BOVIN	Q04973 bos taurus	245	27	77.1	943	1	HIG_DROME	P18330 pseudomonas
173	27	77.1	255	1	PPA1_LYCES	P27061 lycopersico	246	27	77.1	958	1	SVI_ECOLI	Q9101 drosophila
174	27	77.1	263	1	INMT_HUMAN	Q95050 homo sapien	247	27	77.1	1003	1	AV10_HUMAN	Q9hcel homo sapien
175	27	77.1	264	1	NNMT_HUMAN	P40261 homo sapien	248	27	77.1	1066	1	AOSL_PLSHO	O16025 plexaura ho
176	27	77.1	265	1	OTSB_RHISN	P55611 rhizobium s	249	27	77.1	1092	1	DPOD_DROME	P54358 drosophila
177	27	77.1	270	1	TCMP_STRGA	P39887 streptomyce	250	27	77.1	1148	1	POLN_RVVT	P13888 ross river
178	27	77.1	290	1	Y634_XYLFT	Q8vdp8 xyella fas	251	27	77.1	1150	1	NRDC_HUMAN	O43847 homo sapien
179	27	77.1	290	1	YE05_XYLFA	Q9pdh4 xyella fas	252	27	77.1				

253	27	77.1	1157	1	JTP_CABEL	P34609	caenorhabdi	326	26	74.3	261	1	NIF3_HUMAN	Q9gzv7	homo sapien
254	27	77.1	1161	1	NRDC_MOUSE	Q8bhg1	mus musculus	327	26	74.3	261	1	NIF3_MOUSE	P58466	mus musculus
255	27	77.1	1161	1	NRDC_RAT	P47245	rattus norv	328	26	74.3	269	1	NIF3_HUMAN	Q00169	homo sapien
256	27	77.1	1353	1	VGL2_CVHOC	P36334	human coron	329	26	74.3	269	1	PP11_RABIT	P48738	oryctolagus
257	27	77.1	1359	1	STH1_YEAST	P32597	saccharomyc	330	26	74.3	270	1	PP11_MOUSE	P53810	mus musculus
258	27	77.1	1363	1	VGL2_CVBP	P25190	bovine coro	331	26	74.3	270	1	PP11_RAT	P16446	rattus norv
259	27	77.1	1363	1	VGL2_CVBL9	P25191	bovine coro	332	26	74.3	290	1	Y084_MYCBE	P47330	mycoplasma
260	27	77.1	1363	1	VGL2_CVBLY	P25192	bovine coro	333	26	74.3	291	1	SC17_YEAST	P26022	saccharomyc
261	27	77.1	1363	1	VGL2_CVBM	P15777	bovine coro	334	26	74.3	294	1	239F_HUMAN	Q15777	homo sapien
262	27	77.1	1363	1	VGL2_CVBQ	P25193	bovine coro	335	26	74.3	294	1	DAPA_RICTY	Q9ake4	rickettsia
263	27	77.1	1363	1	VGL2_CVBV	P25194	bovine coro	336	26	74.3	294	1	UNG_HSV23	P13158	herpes simp
264	27	77.1	1443	1	DPQ3_MYCPN	P5080	mycoplasma	337	26	74.3	295	1	TSR2_MOUSE	Q8k3v1	mus musculus
265	27	77.1	1499	1	PGP1_HUMAN	Q9y498	homo sapien	338	26	74.3	296	1	CI30_DROME	Q9vail	drosophila
266	27	77.1	1559	1	BPT1_YEAST	P14772	saccharomyc	339	26	74.3	301	1	RPC6_SCHPO	Q94553	schizosacch
267	27	77.1	1638	1	BRM_DROME	P25439	drosophila	340	26	74.3	303	1	SPRC_HUMAN	P09486	homo sapien
268	27	77.1	1947	1	MYSC_CABEL	P12845	caenorhabdi	341	26	74.3	304	1	SPRC_BOVIN	P13213	bos taurus
269	27	77.1	2472	1	SPCN_HUMAN	Q13813	homo sapien	342	26	74.3	305	1	LPXC_ECOLI	P07652	escherichia
270	27	77.1	2472	1	SPCN_RAT	P16086	rattus norv	343	26	74.3	305	1	LPXC_HASIN	P45070	haemophilus
271	27	77.1	2479	1	POLN_RRVN	P13887	ross river	344	26	74.3	305	1	LPXC_PASMU	Q8cpa5	pasteurella
272	27	77.1	3343	1	BRC2_RAT	Q35923	rattus norv	345	26	74.3	305	1	LPXC_SALTU	Q8z9g5	salmonella
273	26	74.3	55	1	SRV_MACEFA	P36391	macaca fasc	346	26	74.3	306	1	LPXC_SALTU	Q8zrt9	salmonella
274	26	74.3	81	1	MOAD_HAEIN	P45309	haemophilus	347	26	74.3	305	1	LPXC_VIBCH	Q8kph2	vibrio chol
275	26	74.3	92	1	Y04B_BP74	P24284	vaccinia vi	348	26	74.3	305	1	LPXC_VIBPA	Q87af9	vibrio para
276	26	74.3	108	1	Y04B_BP74	P07082	bacterioph	349	26	74.3	305	1	LPXC_VIBVU	Q8del6	vibrio vuln
277	26	74.3	113	1	YBBY_ECOLI	P76277	escherichia	350	26	74.3	305	1	TSR2_HUMAN	Q8ney3	homo sapien
278	26	74.3	115	1	Y440_ARCFU	Q29809	archaeoglob	351	26	74.3	306	1	DDL_BUCAP	Q51927	buchnera ap
279	26	74.3	119	1	THH2_BRANA	Q39362	brassica na	352	26	74.3	306	1	LPXC_SHERON	Q8eqg2	shewanella
280	26	74.3	121	1	VNS2_INCAA	Q01640	influenza c	353	26	74.3	306	1	LPXC_YERPE	Q8zie3	yersinia pe
281	26	74.3	121	1	VNS2_INCUJ	P12603	influenza c	354	26	74.3	308	1	ERA_BRAJA	Q69162	bradyrhizob
282	26	74.3	122	1	YHDN_ECOLI	P36677	escherichia	355	26	74.3	309	1	CIWG_HUMAN	Q8et55	homo sapien
283	26	74.3	131	1	HSLR_HAEIN	P44754	haemophilus	356	26	74.3	309	1	KHSE_BACSU	Q49498	bacillus su
284	26	74.3	132	1	HSLR_AERSA	Q44264	aeromonas s	357	26	74.3	310	1	OSAR_HUMAN	Q8ngp9	homo sapien
285	26	74.3	133	1	HSLR_ECOLI	P45802	escherichia	358	26	74.3	310	1	YCF9_YEAST	Q8vgs8	mus musculus
286	26	74.3	133	1	REV_CAEV	P31628	caprine art	359	26	74.3	316	1	YCF9_YEAST	P25586	saccharomyc
287	26	74.3	133	1	REV_CAEV	P33460	caprine art	360	26	74.3	317	1	YB05_VACCO	P24084	vaccinia vi
288	26	74.3	142	1	LYSX_DROME	P37161	drosophila	361	26	74.3	317	1	YB05_VACCC	P24115	vaccinia vi
289	26	74.3	162	1	XYLB_AMFSP	P24271	ampullariel	362	26	74.3	317	1	YB05_VACCV	P24083	vaccinia vi
290	26	74.3	166	1	ING_MARMO	Q35735	marmota mon	363	26	74.3	317	1	YB05_VACCV	Q01227	vaccinia vi
291	26	74.3	167	1	CD3D_SHEEP	P18438	ovis aries	364	26	74.3	319	1	CCSA_OENHO	Q8mt12	oenothera h
292	26	74.3	172	1	Y819_PASMU	Q9cmk4	pasteurella	365	26	74.3	319	1	COBD_BACHD	Q9kci3	bacillus ha
293	26	74.3	176	1	DSBB_ECOLI6	P59343	escherichia	366	26	74.3	319	1	FABG_ARATH	P33207	arabidopsis
294	26	74.3	176	1	DSBB_ECOLI	P30018	escherichia	367	26	74.3	327	1	YG29_SYNY3	P74346	synecocyst
295	26	74.3	176	1	DSBB_SHIFL	Q4155	shigella fl	368	26	74.3	329	1	YCLC_PSEPU	Q47100	pseudomonas
296	26	74.3	176	1	DSBB_YERPE	Q8zemi	yersinia pe	369	26	74.3	334	1	UNG_HSV11	P10186	herpes simp
297	26	74.3	176	1	VA22_VACCC	P20997	vaccinia vi	370	26	74.3	339	1	R13A_ARATH	P3157	a glucan en
298	26	74.3	178	1	E1BS_ADE07	P03248	human adeno	371	26	74.3	339	1	STEA_HUMAN	Q9uhe8	homo sapien
299	26	74.3	181	1	CU25_HUMAN	Q9y426	homo sapien	372	26	74.3	339	1	YTH6_RHOER	P43484	rhodococcus
300	26	74.3	181	1	YCY0_YEAST	P25654	saccharomyc	373	26	74.3	340	1	Y874_CABEL	Q09618	caenorhabdi
301	26	74.3	182	1	Y171_BURCE	P24577	burkholderi	374	26	74.3	340	1	YN93_ANASP	P46079	anabaena sp
302	26	74.3	187	1	VA22_VARV	Q3845	variola vir	375	26	74.3	344	1	PRIS_PYRHO	Q8eqa9	oceanobacil
303	26	74.3	205	1	YB23_METJA	Q58523	methanococ	376	26	74.3	346	1	PRIS_PYRHO	Q57934	pyrococcus
304	26	74.3	206	1	G1DB_YERPE	Q8zr9	yersinia pe	377	26	74.3	347	1	PRIS_PYRPU	Q9p9h1	pyrococcus
305	26	74.3	210	1	G1DB_VIBCH	Q8kng5	vibrio chol	378	26	74.3	350	1	YC73_METJA	Q58669	methanococc
306	26	74.3	211	1	G1DB_VIBPA	Q87k99	vibrio para	379	26	74.3	353	1	RRPO_FVSP	P22657	potato viru
307	26	74.3	211	1	YF78_CABEL	Q92224	caenorhabdi	380	26	74.3	364	1	F16P_XANFL	P23014	xanthobacte
308	26	74.3	212	1	DSBI_SHEON	Q9eam8	shewanella	381	26	74.3	365	1	SOXB_RHOSO	P54997	rhodococcus
309	26	74.3	212	1	RL10_PIG	Q29195	sus scrofa	382	26	74.3	374	1	MTB1_BACBR	P34905	bacillus br
310	26	74.3	213	1	RL10_BOVIN	Q8xh13	bos taurus	383	26	74.3	376	1	KAPR_DROME	P16905	drosophila
311	26	74.3	213	1	RL10_HUMAN	P27635	homo sapien	384	26	74.3	377	1	KAPR_APLCA	P31319	aplysia cal
312	26	74.3	213	1	RL10_MOUSE	P45634	mus musculus	385	26	74.3	378	1	AGAL_COPAR	Q2656	coffea arab
313	26	74.3	223	1	RACE_DICTDI	Q23862	dictyosteli	386	26	74.3	379	1	KAP0_BOVIN	P00514	bos taurus
314	26	74.3	224	1	CTH8_HUMAN	Q9h444	homo sapien	387	26	74.3	379	1	KAP0_PIG	P07802	sus scrofa
315	26	74.3	224	1	CTH8_MOUSE	Q8d8b3	mus musculus	388	26	74.3	380	1	KAP0_RAT	P09456	rattus norv
316	26	74.3	226	1	SP25_CANFA	Q28250	canis famil	389	26	74.3	381	1	KAP0_HUMAN	P10644	homo sapien
317	26	74.3	226	1	SP25_HUMAN	Q15005	homo sapien	390	26	74.3	384	1	CGB3_CABEL	Q10654	caenorhabdi
318	26	74.3	226	1	SP25_MOUSE	Q2cyn2	mus musculus	391	26	74.3	385	1	DXR1_BACAA	Q8n10	basillus an
319	26	74.3	228	1	RNFG_PSEST	Q9evn3	pseudomonas	392	26	74.3	385	1	DXR1_BACBR	Q81b49	basillus ce
320	26	74.3	229	1	UNG_COXBU	Q83cw4	coxiella bu	393	26	74.3	385	1	YM30_MYCLE	O69481	mycobacteri
321	26	74.3	230	1	ALKL_PSEOL	Q00595	pseudomonas	394	26	74.3	388	1	PURK_SYNY3	P74724	synecocyst
322	26	74.3	250	1	PECB_SCHGR	P82886	schistocerc	395	26	74.3	389	1	GALT_BUTFI	P45981	butyrivibri
323	26	74.3	250	1	AGGD_ECOLI	P46004	escherichia	396	26	74.3	394	1	TYRB_PARDE	P95468	paracoccus
324	26	74.3	255	1	RECO_LISTIN	Q22bq0	listeria in	397	26	74.3	397	1	ASSY_XANCP	Q8p8j4	xanthomonas
325	26	74.3	255	1	UNG_HSV2H	P28275	herpes simp	398	26	74.3	408	1	EFTU_GUITH	P19457	guillardia

399	26	74.3	411	1	AGAL_CVATE
400	26	74.3	411	1	VG66_HSV11
401	26	74.3	412	1	ASSY_XANAC
402	26	74.3	413	1	AMP2_BACST
403	26	74.3	413	1	STAL_CHICK
404	26	74.3	414	1	MTNW_BACSU
405	26	74.3	420	1	RBL_PYRFU
406	26	74.3	424	1	RBL_PYRAB
407	26	74.3	429	1	PEPB_VIBCH
408	26	74.3	432	1	PEPB_VIBPA
409	26	74.3	432	1	R114_SACPA
410	26	74.3	433	1	W023_FOWPV
411	26	74.3	434	1	DHE4_HALSA
412	26	74.3	435	1	R114_YEAST
413	26	74.3	437	1	ENCB_VIBVU
414	26	74.3	439	1	SYE2_HELPJ
415	26	74.3	443	1	CSN2_HUMAN
416	26	74.3	453	1	KYN2_YEAST
417	26	74.3	459	1	KGPF_THELI
418	26	74.3	465	1	HNFB_HUMAN
419	26	74.3	465	1	HNFB_MOUSE
420	26	74.3	465	1	HNFB_RAT
421	26	74.3	471	1	GATH_SCHPO
422	26	74.3	471	1	RCA_SPIOL
423	26	74.3	475	1	YMT4_YEAST
424	26	74.3	480	1	AGLA_THEMA
425	26	74.3	482	1	PCD7_MOUSE
426	26	74.3	485	1	PCD7_HUMAN
427	26	74.3	487	1	DPD2_YEAST
428	26	74.3	487	1	YFGC_ECO57
429	26	74.3	487	1	YFGC_ECOLI
430	26	74.3	490	1	C883_ARATH
431	26	74.3	493	1	GLO3_YEAST
432	26	74.3	494	1	SYE_PSEAE
433	26	74.3	496	1	PCP_HUMAN
434	26	74.3	499	1	ABFB_ASPNG
435	26	74.3	500	1	DPD2_RAT
436	26	74.3	502	1	LAS1_YEAST
437	26	74.3	504	1	CP42_YEAST
438	26	74.3	504	1	YM68_YEAST
439	26	74.3	506	1	DPF2_MOUSE
440	26	74.3	507	1	CP43_RAT
441	26	74.3	507	1	EPOR_MOUSE
442	26	74.3	508	1	CP48_RAT
443	26	74.3	508	1	EPOR_HUMAN
444	26	74.3	509	1	CP41_RAT
445	26	74.3	509	1	Y795_HUMAN
446	26	74.3	510	1	CP46_RABIT
447	26	74.3	511	1	CP45_RABIT
448	26	74.3	511	1	CP4B_HUMAN
449	26	74.3	511	1	CP4B_MOUSE
450	26	74.3	511	1	CP4B_RAT
451	26	74.3	511	1	U171_CAEL
452	26	74.3	512	1	ALDB_ECOLI
453	26	74.3	519	1	CP4Y_HUMAN
454	26	74.3	524	1	CPFC_HUMAN
455	26	74.3	529	1	CN1A_BOVIN
456	26	74.3	532	1	CSI_NEUCR
457	26	74.3	534	1	CN1A_HUMAN
458	26	74.3	538	1	TCMA_STRGA
459	26	74.3	545	1	AMDS_ASPOR
460	26	74.3	545	1	CP10_LYMTS
461	26	74.3	547	1	YOJ1_ECOLI
462	26	74.3	551	1	CBX4_MOUSE
463	26	74.3	551	1	OPGD_SALTI
464	26	74.3	551	1	OPGD_SALTY
465	26	74.3	552	1	YGBX_BACSU
466	26	74.3	558	1	CBX4_HUMAN
467	26	74.3	558	1	VB04_VARV
468	26	74.3	566	1	SYRD_PSESY
469	26	74.3	573	1	DPOL_MOUSE
470	26	74.3	575	1	VP05_BFT4
471	26	74.3	575	1	VP05_BFT4

472	26	74.3	582	1	VATA_DEIRA
473	26	74.3	587	1	GGT_BACSU
474	26	74.3	589	1	C49A_DROME
475	26	74.3	590	1	SYD_SALTI
476	26	74.3	590	1	SYD_SALTY
477	26	74.3	591	1	SYR_BORBU
478	26	74.3	592	1	SVC2_RAT
479	26	74.3	593	1	GRN_HUMAN
480	26	74.3	600	1	GLMS_STAAM
481	26	74.3	600	1	GLMS_STAAM
482	26	74.3	607	1	VATA_NEUCR
483	26	74.3	619	1	MUTL_XYLFA
484	26	74.3	619	1	MUTL_XYLFT
485	26	74.3	620	1	ACE1_CAEER
486	26	74.3	620	1	ACE1_CAEEL
487	26	74.3	620	1	KHL8_HUMAN
488	26	74.3	623	1	PTR2_CANAL
489	26	74.3	624	1	MUTL_XANCP
490	26	74.3	624	1	PTWA_PASMU
491	26	74.3	629	1	KHL8_MOUSE
492	26	74.3	633	1	GYP3_YEAST
493	26	74.3	647	1	SVC2_MOUSE
494	26	74.3	650	1	SVC2_HUMAN
495	26	74.3	660	1	DNLJ_CHIMU
496	26	74.3	686	1	KITH_HSVBM
497	26	74.3	691	1	YHJG_ECOLI
498	26	74.3	692	1	RFK2_MOUSE
499	26	74.3	701	1	YL66_YEAST
500	26	74.3	709	1	CNIC_HUMAN

ALIGNMENTS

RESULT 1
 KYN RAT
 ID KYN RAT STANDARD; PRT; 464 AA.
 AC P70712; Q9QW90;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Kynureninase (EC 3.7.1.3) (L-kynurenine hydrolase).
 GN KYN.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;
 [1]

SEQUENCE, AND MASS SPECTROMETRY.

STRAIN=Wistar; TISSUE=Liver;
 RC MEDLINE=96049498; PubMed=7578221;
 RA Takeuchi F., Tsubouchi R., Yoshino M., Shibata Y.;
 "Amino-acid sequence of rat liver kynureninase.";
 Biochim. Biophys. Acta 1252:185-188(1995).
 [2]

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

TISSUE=Liver;
 RC MEDLINE=97324088; PubMed=9180257;
 RA Tona S., Nakamura M., Tone S., Okuno E., Kido R., Breton J.,
 Avanzi N., Cozzi L., Speciale C., Mostardini M., Gatti S., Benatti L.;
 "Cloning and recombinant expression of rat and human kynureninase.";
 FEBS Lett. 408:5-10(1997).
 [3]

SEQUENCE OF 19-117 FROM N.A., AND PARTIAL SEQUENCE.

TISSUE=Kidney, and Liver;
 RC MEDLINE=963114506; PubMed=8706755;
 RA Alberati-Giani D., Buchli R., Malherbe P., Broger C., Lang G.,
 Koehler C., Lahm H.-W., Cesura A.M.;
 "Isolation and expression of a cDNA clone encoding human
 kynureninase.";
 Eur. J. Biochem. 239:460-468(1996).
 CC -I- FUNCTION: Catalyzes the cleavage of L-kynurenine (L-KYN) and L-3-
 hydroxykynurenine (L-3OHKYN) into anthranilic (AA) and 3-

hydroxyanthranilic acids (3-OHAA), respectively. Has a preference for the L-3-hydroxy form. Optimum activity is around pH 9.0 for L-kyn and around 8.5 for L-3OHKYN. Also has cysteine-conjugate-beta-lyase activity.

-1- CATALYTIC ACTIVITY: L-kynurenine + H(2)O = anthranilate + L-alanine.

-1- CATALYTIC ACTIVITY: L-3-hydroxykynurenine + H(2)O = 3-hydroxyanthranilate + L-alanine.

-1- COFACTOR: Pyridoxal phosphate.

-1- ENZYME REGULATION: Inhibited by o-methylbenzoylalanine (OMBA).

-1- PATHWAY: Involved in the biosynthesis of NAD cofactors from tryptophan through the kynurenine pathway.

-1- SUBUNIT: Homodimer.

-1- TISSUE SPECIFICITY: High levels in liver and kidney. Also detected in heart, retina, ovary, lung, testis and brain.

-1- INDUCTION: Inhibited by thiol reagents and heavy metal ions.

-1- SIMILARITY: BELONGS TO THE KYURENINASE FAMILY. SLIGHTLY RELATED TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; U68168; AAC53206.1; -

PIR; S59898; S59898.

PIR; T48675; T48675.

KW Hydroxylase; Pyridoxal phosphate; Acetylation.

FT MOD RES 1 1 ACETYLATION.

FT BINDING 276 276 PYRIDOXAL PHOSPHATE.

FT CONFLICT 18 18 A -> T (IN REF. 1).

FT CONFLICT 26 26 D -> N (IN REF. 1).

FT CONFLICT 118 118 T -> S (IN REF. 1).

SQ SEQUENCE 464 AA; 52453 MW; F1FC95E3202CECC CRC64;

Query Match 100.0%; Score 35; DB 1; Length 464;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ELDKWA 6

Db 90 ELDKWA 95

RESULT 2

KYNU HUMAN

ID KYNU HUMAN STANDARD; PRT; 465 AA.

AC Q16719;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Kynureninase (EC 3.7.1.3) (L-kynurenine hydrolase).

GN KYNU.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RN SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC TISSUE=Hepatoma;

RA MEDLINE=96314506; PubMed=8706755;

RA Alberati-Giani D., Buchli R., Malherbe P., Broger C., Lang G., Koehler C., Lahm H.-W., Cesura A.M.;

RT "Isolation and expression of a cDNA clone encoding human kynureninase."

RL Eur. J. Biochem. 239:460-468(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=97324088; PubMed=9180257;

RA Toma S., Nakamura M., Tone S., Okuno E., Kido R., Breton J., Avanzi N., Cozzi L., Speciale C., Mostardini M., Gatti S., Benatti L.;

RT "Cloning and recombinant expression of rat and human kynureninase.";

RL FEBS Lett. 408:5-10(1997).

CC -1- FUNCTION: Catalyzes the cleavage of L-kynurenine (L-KYN) and L-3-hydroxykynurenine (L-3OHKYN) into anthranilic (AA) and 3-hydroxyanthranilic acids (3-OHAA), respectively. Has a preference for the L-3-hydroxy form. Also has cysteine-conjugate-beta-lyase activity (By similarity).

CC -1- CATALYTIC ACTIVITY: L-kynurenine + H(2)O = anthranilate + L-alanine.

CC -1- CATALYTIC ACTIVITY: L-3-hydroxykynurenine + H(2)O = 3-hydroxyanthranilate + L-alanine.

CC -1- COFACTOR: Pyridoxal phosphate.

CC -1- ENZYME REGULATION: Inhibited by o-methoxybenzoylalanine (OMBA).

CC -1- PATHWAY: Involved in the biosynthesis of NAD cofactors from tryptophan through the kynurenine pathway.

CC -1- SUBUNIT: Homodimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- TISSUE SPECIFICITY: Expressed in all tissues tested (heart, brain placenta, lung, liver, skeletal muscle, kidney and pancreas).

CC Highest levels found in placenta, liver and lung. Expressed in all brain regions.

CC -1- INDUCTION: Increased levels in several cerebral and systemic inflammatory conditions.

CC -1- SIMILARITY: BELONGS TO THE KYURENINASE FAMILY. SLIGHTLY RELATED TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; U57721; AAC50650.1; -

PIR; G02652; G02652.

Genew; HGNC:6469; KYNU.

GK; Q16719; -

MM; 605197; -

MM; 236800; -

GO; GO:0008233; F:peptidase activity; TAS.

GO; GO:0008233; F:peptidase activity; Acetylation.

KW Hydroxylase; Pyridoxal phosphate; Acetylation.

FT MOD RES 1 1 ACETYLATION (BY SIMILARITY).

FT BINDING 276 276 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

SQ SEQUENCE 465 AA; 52351 MW; BDD136BE18C79EBB CRC64;

Query Match 100.0%; Score 35; DB 1; Length 465;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ELDKWA 6

Db 90 ELDKWA 95

RESULT 3

YR86 CAEEL

ID YR86 CAEEL STANDARD; PRT; 817 AA.

AC Q09568;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypothetical protein F4888.6 in chromosome III.

GN F4888.6.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

```

RC STRAIN-Bristol N2;
RA Kirsten J.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ribonuclease II (RNB) family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U23514; AAC4543.1; -.
DR PIR; T16409; T16409.
DR WormPep; F48E8.6; CE02758.
DR InterPro; IPR001900; Ribonuclease_II.
DR Pfam; PF00773; RNB; 1.
DR PROSITE; PS01175; RIBONUCLEASE_II; 1.
KW Hypothetical protein; Hydrolase; Nuclease.
SQ SEQUENCE 817 AA; 93727 MW; 9BE5B06162699243 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 817;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 359 ELDKWA 364
|||||

RESULT 4
ENV_HV1ND STANDARD; PRT; 846 AA.
ID -ENV_HV1ND
AC P18799;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11695;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=90034200; PubMed=2806917;
RA Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F.,
RA Hampe A., Chermann J.C.;
RT "Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the
RT human immunodeficiency virus.";
RL Gene 81:275-284(1989).
CC -1- MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH
CC AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M27323; AAA44873.1; -.
DR PIR; JQ0066; VCLJND.
DR HIV; M27323; ENV5NDK.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00317; GP41; 1.
KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL
  
```

```

FT CHAIN 30 501
FT CHAIN 502 846
FT DISULFID 53 73
FT DISULFID 118 200
FT DISULFID 125 191
FT DISULFID 130 152
FT DISULFID 213 242
FT DISULFID 223 234
FT DISULFID 291 328
FT DISULFID 374 435
FT DISULFID 381 408
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 151 151
FT CARBOHYD 179 179
FT CARBOHYD 182 182
FT CARBOHYD 229 229
FT CARBOHYD 236 236
FT CARBOHYD 257 257
FT CARBOHYD 271 271
FT CARBOHYD 284 284
FT CARBOHYD 290 290
FT CARBOHYD 351 351
FT CARBOHYD 382 382
FT CARBOHYD 388 388
FT CARBOHYD 392 392
FT CARBOHYD 395 395
FT CARBOHYD 401 401
FT CARBOHYD 438 438
FT CARBOHYD 451 451
FT CARBOHYD 452 452
FT CARBOHYD 601 601
FT CARBOHYD 606 606
FT CARBOHYD 615 615
FT CARBOHYD 627 627
SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DA527DE2B83 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 846;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 652 ELDKWA 657
|||||

RESULT 5
ENV_HV1S1 STANDARD; PRT; 847 AA.
ID -ENV_HV1S1
AC P19550;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398(1990).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
  
```


FT DISULFID 378 440 BY SIMILARITY. (POTENTIAL).
 FT DISULFID 385 413 BY SIMILARITY. (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 632 632 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 745 745 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 811 811 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 851;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ELDKWA 6
 Db 657 ELDKWA 662
 RESULT 9
 ENV_HV18N STANDARD; PRT; 852 AA.
 AC P12488;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89085613; PubMed=2789516;
 RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P., Dandekar S.;
 RA "Biological and molecular characterization of human immunodeficiency virus (HIV-1BR) from the brain of a patient with progressive dementia.";
 RT Virology 168:79-89 (1989).
 RL -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>)

or send an email to license@isb-sib.ch.
 CC EMBL; M21098; AAA44221.1; -.
 CC PIR; A31667; VCLJBR.
 DR PDB; 1IM7; 23-OCT-02.
 DR HIV; M21098; ENV\$BRVA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 31 507 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 508 852 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 155 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 330 BY SIMILARITY.
 FT DISULFID 376 439 BY SIMILARITY.
 FT DISULFID 383 412 BY SIMILARITY.
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 670 670 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 852 AA; 97203 MW; 2BB866345DEC915F CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 852;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ELDKWA 6
 Db 658 ELDKWA 663
 RESULT 10
 ENV_HV18N STANDARD; PRT; 852 AA.
 AC P19549;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range, region of
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome.";
RL J. Virol. 64:4016-4020(1990).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY352275; AAQ17031.1; -;
DR PDB; 1MEQ; 11-DEC-02.
DR HIV; M38427; ENV\$SF33.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 156 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 237 331 BY SIMILARITY.
FT DISULFID 377 439 BY SIMILARITY.
FT DISULFID 384 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 852 AA; 96663 MW; EE7BBF8D23C9910D CRC64;

Query Match 100.0%; Score 35; DB 1; Length 852;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 658 ELDKWA 663
RESULT 11
ENV_HV1EL STANDARD; PRT; 853 AA.
ID AC P04581;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BLI isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; PubMed=2424612;
RA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
RT of two isolates from African patients.";
RL Cell 46:63-74(1986).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K03454; AAA44329.1; -;
DR EMBL; A07108; CAA00616.1; -;
DR HIV; K03454; ENV\$ELI.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).


```

FT CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96721 MW; F9CD864DAA0D07A5 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 853;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 659 ELDKWA 664

RESULT 12
ENV_HVMP
ID -ENV_HVMP STANDARD; PRT; 853 AA.
AC P19551;
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11704;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317877; PubMed=1695254;
RA Stevenson M., Haggerty S., Lamonic C., Mann A.M., Meier C.,
RA Wasia A.
RT "Cloning and characterization of human immunodeficiency virus type 1
RT variants diminished in the ability to induce syncytium-independent
RT cytolysis.";
RL J. Virol. 64:3792-3803 (1990).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M33943; AAA44850.1; -.
CC PDB; 1AIK; 16-JUN-97.
CC HIV; M33943; ENV$MFA.
CC InterPro; IPR000328; ENV GP41.
CC InterPro; IPR000777; GP120.
CC Pfam; PF00516; GP120; 1.
CC Pfam; PF00517; GP41; 1.
CC AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
CC 3D-structure.
CC SIGNAL 1 30
CC CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
CC CHAIN 510 853 TRANSMEMBRANE GLYCOPROTEIN.
CC DISULFID 54 74 BY SIMILARITY.
CC DISULFID 119 203 BY SIMILARITY.

```

```

FT DISULFID 126 194 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 226 245 BY SIMILARITY.
FT DISULFID 294 329 BY SIMILARITY.
FT DISULFID 376 443 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 337B993B6F22ABA CRC64;

Query Match 100.0%; Score 35; DB 1; Length 853;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 660 ELDKWA 665

RESULT 13
ENV_HV122
ID -ENV_HV122 STANDARD; PRT; 853 AA.
AC P12487;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11683;
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RA Submitted (NOV-1986) to the HIV data bank.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC

```

[illegible][illegible]

FT	CARBOHYD	294	294	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	300	300	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	306	306	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	336	336	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	359	359	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	389	389	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	395	395	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	399	399	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	405	405	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	610	610	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	615	615	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	636	636	N-LINKED (GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	815	815	N-LINKED (GLCNAC. .)	(POTENTIAL).
SQ	SEQUENCE	855 AA;	97476 MW; 9CF82A607ADD62DA CRC64;		

Query Match 100.0%; Score 35; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 ELDKWA 6 	
Db	661 ELDKWA 666	

```

RESULT 16
ID ENV_HV126 STANDARD; PRT; 855 AA.
AC P04560;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DE ENV.
GS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11708;
OX [1]
RN RN SEQUENCE FROM N.A.
RP MEDLINE=87248097; PubMed=3036660;
RX Srinivasan A., Anand R., York D., Ranganathan P., Peorino P., RA Schochetman G., Curran J., Kalyanaram V.S., Luciw P.A., RA Sanchez-Pescador R.;
RT "Molecular characterization of human immunodeficiency virus from Zaire: nucleotide sequence analysis identifies conserved and variable domains in the envelope gene.";
RT Gene 52:71-82(1987).
RL CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K03458; AAA45380.1; --
DR FIR; D26192; VCLJZR.
DR HIV; K03458; ENV526.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00317; GP41; 1.
DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
KW SIGNAL.
FT FT 1 30
FT CHAIN 31 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 511 855 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 207 BY SIMILARITY.
FT DISULFID 125 198 BY SIMILARITY.
```


Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 662 ELDKWA 667

RESULT 18

```

ENV_HV1H2
ID _ENV HV1H2 STANDARD; PRT; 856 AA.
AC P04578; C09779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69 (1987).
RN [2]
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
Gallo R.C., Wong-Staal F.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K03455; AAB50262.1; -.
DR EMBL; AF038399; AAB99976.1; -.
DR EMBL; AF038119; AAC82596.1; -.
DR PDB; 1DF4; 26-JAN-00.
DR PDB; 1DF5; 26-JAN-00.
DR PDB; 1DLB; 02-APR-00.
DR PDB; 1G9M; 27-DEC-00.
DR PDB; 1GCI; 19-AUG-98.
DR PDB; 1GZL; 10-OCT-02.
DR PDB; 1K33; 10-OCT-01.
DR PDB; 1K34; 10-OCT-01.
DR HIV; K03455; ENVSHXB2.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR00777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
3D-structure.
FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 31 511 TRANSMEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.

```

```

FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97212 MW; 6PAB16AF85107F80 CRC64;

```

Query Match 100.0%; Score 35; DB 1; Length 856;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 662 ELDKWA 667

RESULT 19

```

ENV_HV1H3
ID _ENV HV1H3 STANDARD; PRT; 856 AA.
AC P04624;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11707;
RN [1]
RP SEQUENCE FROM N.A.
RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
Shaw G.M., Wong-Staal F., Reddy E.P.;
RT "HTLV-III env gene products synthesized in E. coli are recognized by
antibodies present in the sera of AIDS patients.";
RL Cell 41:979-986 (1985).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M14100; AAA44679.1; -.

```



```

Query Match      100.0%; Score 35; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ELDKWA 6
Db      662 ELDKWA 667

RESULT 21
ENV_HV1NPV
ID - ENV HV1NPV STANDARD; PRT; 856 AA.
AC P05877;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11696;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal P., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988)
CC -1 - MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC PATIENT IN 1984.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M17449; AAA44857.1; -.
DR PDB; 1ACY; 31-JUL-94.
DR PDB; 1F58; 29-DEC-99.
DR PDB; 1N1Z; 25-FEB-03.
DR PDB; 1NJ0; 25-FEB-03.
DR HIV; M17449; ENVSMN.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 513 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 514 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 210 BY SIMILARITY.
FT DISULFID 125 201 BY SIMILARITY.
FT DISULFID 130 162 BY SIMILARITY.
FT DISULFID 223 252 BY SIMILARITY.
FT DISULFID 233 244 BY SIMILARITY.
FT DISULFID 301 335 BY SIMILARITY.
FT DISULFID 381 445 BY SIMILARITY.
FT DISULFID 388 418 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).

```

```

FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 343 343 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 626 626 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 638 638 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97140 MW; D197D809940BE732 CRC64;

Query Match      100.0%; Score 35; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ELDKWA 6
Db      663 ELDKWA 668

RESULT 22
ENV_HV1NPV
ID - ENV HV1NPV STANDARD; PRT; 856 AA.
AC P03376;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Laeky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; K02083; BAB59873.1; -.
DR EMBL; X01762; CAA25903.1; ALT_SEQ.
DR PIR; A03974; VCLJVL.
DR HIV; K02083; ENVSPV22.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.

```


Db 662 ELDKWA 667

RESULT 24

ENV_HV1M1 STANDARD; PRT; 856 AA.

AC P31872; (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 10-JUL-1993 (Rel. 26, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (HIV-1) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=31678;

RN [1]

RP MEDLINE=86218077; PubMed=2423350;

RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;

RT "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS."

RT AIDS; 4:637-648(1986).

RL Cell 45:637-648(1986).

CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.

CC PIR; A24774; VCLJ3W

DR PDB; 1LB0; 04-DEC-02.

DR PDB; 1LCX; 04-DEC-02.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal; 3D-structure.

KW SIGNAL 1 29

FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 205 BY SIMILARITY.

FT DISULFID 125 196 BY SIMILARITY.

FT DISULFID 130 152 BY SIMILARITY.

FT DISULFID 218 247 BY SIMILARITY.

FT DISULFID 228 239 BY SIMILARITY.

FT DISULFID 296 330 BY SIMILARITY.

FT DISULFID 376 444 BY SIMILARITY.

FT DISULFID 383 417 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 856 AA; 97526 MW; DB68D1E49C404DE9 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 856;

Best Local Similarity 100.0%; Pred. No; 20;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6

Db 662 ELDKWA 667

RESULT 25

ENV_HV1M1 STANDARD; PRT; 859 AA.

AC P04583;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11697;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=86245056; PubMed=2424612;

RA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;

RT "Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients."

RL Cell 46:63-74(1986).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; X04415; CAA28016.1; -.

DR EMBL; A07116; CAA00623.1; -.

DR PIR; T01672; T01672.

DR HIV; K03456; ENVSMAL.

DR InterPro; IPR000328; Env GP41.

DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 31 513 TRANSMEMBRANE GLYCOPROTEIN.

FT CHAIN 514 859 BY SIMILARITY.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 210 BY SIMILARITY.

FT DISULFID 125 201 BY SIMILARITY.

FT DISULFID 130 162 BY SIMILARITY.

FT DISULFID 223 252 BY SIMILARITY.

FT DISULFID 233 244 BY SIMILARITY.

FT DISULFID 301 334 BY SIMILARITY.

FT DISULFID 380 445 BY SIMILARITY.

FT DISULFID 387 418 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 357 357 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 819 819 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 859 AA; 97109 MW; DBCF9AAS2E3ABF29 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 859;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
Db 664 ELDKWA 669
|||||

RESULT 26
ENV_HVIRH STANDARD; PRT; 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11866;
RN [1]
RP MEDLINE=85099333; PubMed=2981635;
RA Wain-Hobson S., Sonigo P., Dancos O., Cole S., Alizon M.;
RT "Nucleotide sequence of the AIDS virus, LAV.";
RL Cell 40:9-17(1985).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL; K02013; AAB59751.1; -
DR EMBL; A04321; CAA00352.1; -
DR PIR; A03975; VCLJLV.
DR FDB; IERF; 20-FEB-02.
DR HIV; K02013; ENV\$BRU.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
3D-structure. 1 30
FT SIGNAL 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 517 861 TRANSMEMBRANE GLYCOPROTEIN.
FT

FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 210 BY SIMILARITY.
FT DISULFID 126 201 BY SIMILARITY.
FT DISULFID 131 162 BY SIMILARITY.
FT DISULFID 223 252 BY SIMILARITY.
FT DISULFID 233 244 BY SIMILARITY.
FT DISULFID 301 336 BY SIMILARITY.
FT DISULFID 383 450 BY SIMILARITY.
FT DISULFID 390 423 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 630 630 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 642 642 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 679 679 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 755 755 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 821 821 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 861 AA; 97487 MW; 04DE2B4D4E4FD63A CRC64;

Query Match 100.0%; Score 35; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
Db 667 ELDKWA 672
|||||

RESULT 27
ENV_HVIRH STANDARD; PRT; 865 AA.
AC P04579;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11701;
RN [1]
RP MEDLINE=86218077; PubMed=2423250;
RA Starck B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal P.;
RT "Identification and characterization of conserved and variable
regions in the envelope gene of HTLV-III/LAV, the retrovirus of
AIDS.";
RT

```

Cell 45:637-648(1986).
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; M17451; AAA45057.1; -.
HIV; M17451; ENVSRF.
InterPro; IPR000328; Env GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
Signal.
CHAIN 1 29
CHAIN 30 519
CHAIN 520 865
DISULFID 53 73
DISULFID 118 218
DISULFID 125 209
DISULFID 130 157
DISULFID 231 260
DISULFID 241 252
DISULFID 309 343
DISULFID 389 452
DISULFID 396 425
CARBOHYD 87 87
CARBOHYD 129 129
CARBOHYD 136 136
CARBOHYD 139 139
CARBOHYD 156 156
CARBOHYD 193 193
CARBOHYD 194 194
CARBOHYD 197 197
CARBOHYD 198 198
CARBOHYD 203 203
CARBOHYD 210 210
CARBOHYD 247 247
CARBOHYD 254 254
CARBOHYD 275 275
CARBOHYD 289 289
CARBOHYD 302 302
CARBOHYD 308 308
CARBOHYD 314 314
CARBOHYD 344 344
CARBOHYD 351 351
CARBOHYD 367 367
CARBOHYD 397 397
CARBOHYD 403 403
CARBOHYD 407 407
CARBOHYD 413 413
CARBOHYD 418 418
CARBOHYD 455 455
CARBOHYD 471 471
CARBOHYD 620 620
CARBOHYD 625 625
CARBOHYD 634 634
CARBOHYD 646 646
CARBOHYD 825 825
SEQUENCE 865 AA; 97809 MW; 28828BC211ADCAC CRC64;
Query Match 100.0%; Score 35; DB 1; Length 865;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 671 ELDKWA 676

```

RESULT 28

```

NIA_SPIOL
ID NIA_SPIOL STANDARD; PRT; 926 AA.
AC P23312; 041377;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] [EC 1.7.1.1] (NR).
GN NIA.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=91355858; PubMed=2103436;
RA Prosser I.M., Lazarus C.M.;
RL Plant Mol. Biol. 15:187-190(1990).
[2]
RN RP SEQUENCE FROM N.A.
RX STRAIN=cv. Hoyo;
RA MEDLINE=97273959; PubMed=9128133;
RA Tamura N., Takahashi H., Takeba G., Satoi T., Nakagawa H.;
RT "The nitrate reductase gene isolated from DNA of cultured spinach
RT cells.";
RL Biochim. Biophys. Acta 1338:151-155(1997).
[3]
RN RP SEQUENCE OF 287-926 FROM N.A.
RX STRAIN=cv. Hoyo;
RA Shiraiishi N., Kubo Y., Takeba K., Kiyota S., Sakano K., Nakagawa H.;
RT "Sequence analysis of cloned cDNA and proteolytic fragments for
RT nitrate reductase from Spinacia oleracea L.";
RL Plant Cell Physiol. 32:1031-1038(1991).
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -!- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD,
CC heme iron, and molybdenum-pterin as prosthetic groups. The heme
CC group is called cytochrome b-557.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; M32600; AAA34033.1; -.
EMBL; D86226; BAA13047.1; -.
EMBL; U08029; AAA18377.1; -.
PIR; S11868; RDSPNH.
HSP; P17571; 2CND.
InterPro; IPR001199; Cyt B5.
InterPro; IPR001834; Cyt_B5_reductase.
InterPro; IPR008335; Ruk_Mb_oxred.
InterPro; IPR008333; FAD_binding_6.
InterPro; IPR001709; PFN_cyt_redctse.
InterPro; IPR007110; Ig-like.
InterPro; IPR005066; Mo-co_dimer.
InterPro; IPR000572; Oxidored_molyb.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00970; FAD_binding_6; 1.
Pfam; PF00173; heme_1; 1.

```

```
DR Pfam; PF03404; Mo-co dimer; 1.
DR Pfam; PF00175; NAD binding 1; 1.
DR Pfam; PF00174; oxidored molyb; 1.
DR PRINTS; PR00406; CYTBSRDTASE.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PRODom; PD000612; Cyt B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS02255; CYTOCHROME B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation.
KW METAL 204 204 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 258 258 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 443 443 INTERCHAIN (POTENTIAL).
FT METAL 586 586 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 609 609 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 303 303 D -> A (IN REF. 2).
SQ SEQUENCE 926 AA; 103970 MW; FF21DF01963FLAFC CRC64;

Query Match 100.0%; Score 35; DB 1; Length 926;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 845 ELDKWA 850

RESULT 29
Y067 CHLTR
ID Y067 CHLTR STANDARD; PRT; 326 AA.
AC Q95529; O84070;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative metal-binding lipoprotein Ctp067 precursor.
GN Ctp067.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2/434/Bu;
RX MEDLINE=99392470; PubMed=10463174;
RA Bannantine J.P., Rockett D.D.;
RT "Use of primate model system to identify Chlamydia trachomatis protein
antigens recognized uniquely in the context of infection.";
RL Microbiology 145:2077-2085(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/Cx;
RX MEDLINE=9900809; PubMed=9784136;
RA Stephens R.S., Kallan S., Lammell C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -!- FUNCTION: PART OF AN ATP-DRIVEN TRANSPORT SYSTEM
CT067/CT068/CT069/CT070 FOR A METAL. METAL-BINDING COMPONENT.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(Possible).
CC -!- SIMILARITY: Belongs to the bacterial solute-binding protein family
9.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/)
or send an email to license@isb-sib.ch.
CC
```

```
CC or send an email to license@isb-sib.ch.
CC EMBL; AF077010; AAC35948.1; ALT_INIT.
DR EMBL; AE001281; AAC67658.1; -.
DR PIR; E71561; E71561.
DR FIC1-2DPAGE; Q98529; -.
DR InterPro; IPR006128; Lipoprotein 4.
DR InterPro; IPR006127; SBP_bac_9.
DR Pfam; PF01297; SBP_bac_9; 1.
DR PRINTS; PR00690; ADHESNFAMILY.
KW Hypothetical protein; Transport; Metal-binding; Lipoprotein; Membrane;
KW Signal; Complete proteome; Palmitate.
FT SIGNAL 1 21 PROBABLE.
FT CHAIN 22 326 PUTATIVE METAL-BINDING LIPOPROTEIN
CT067.
FT LIPID 22 22 N-palmitoyl cysteine (Probable).
FT LIPID 22 22 S-diacylglycerol cysteine (Probable).
FT VARIANT 190 190 A -> V (IN SEROVAR L2).
SQ SEQUENCE 326 AA; 37035 MW; 5ASAA35AB6627D89 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 326;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 184 ELDRWA 189

RESULT 30
LGT_TREPA
ID LGT_TREPA STANDARD; PRT; 332 AA.
AC O83824;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-).
GN LGT OR TP0852.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
spirochete.";
RL Science 281:375-388(1998).
CC -!- FUNCTION: Transfers the N-acyl diglyceride group on what will
become the N-terminal cysteine of membrane lipoproteins.
CC -!- PATHWAY: Lipoproteins biosynthesis; first step.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -!- SIMILARITY: Belongs to the lgt family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/)
or send an email to license@isb-sib.ch.
CC
CC EMBL; AE001255; AAC65817.1; -.
DR PIR; D71274; D71274.
DR TIGR; TP0852; -.
DR InterPro; IPR001640; LGT.
```

```

DR Pfam; PF01790; LGT; 1.
DR ProDom; PD005412; LGT; 1.
DR TIGRFAMs; TIGR00544; LGT; 1.
DR PROSITE; PS01311; LGT; 1.
KW Transferase; Transmembrane; Inner membrane; Complete proteome.
FT TRANSFERASE 19 39
FT TRANSMEM 66 86
FT TRANSMEM 111 131
FT TRANSMEM 172 192
FT TRANSMEM 221 241
FT TRANSMEM 249 269
FT TRANSMEM 302 322
FT TRANSMEM 332 352
SQ SEQUENCE 332 AA; 38154 MW; 6FD260564892269D CRC64;

Query Match          91.4%; Score 32; DB 1; Length 332;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 47 ELDKWS 52

RESULT 31
T2S1_STRAH          STANDARD;          PRT;          358 AA.
AC O31074;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Type II restriction enzyme SacI (EC 3.1.21.4) (Endonuclease SacI)
DE (R.SacI).
GN SACI.
OS Streptomyces achromogenes.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=67255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12767;
RX MEDLINE=99077292; PubMed=9862476;
RA Xu S.-Y., Xiao J.-P., Ettwiller L., Holden M., Aliotta J., Poh C.L.,
RA Dalton M., Robinson D.P., Petronzio T.R., Moran L., Ganatra M.,
RA Ware J., Slatko B., Benner J. II;
RT "Cloning and expression of the ApaLI, NspI, NspHI, SacI, ScaI, and
RT SapI restriction-modification systems in Escherichia coli.";
RL Mol. Gen. Genet. 260:226-231(1998).
CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GAGCTC AND
CC CLEAVES AFTER T-5.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/ebis-sib.ch/announce/
CC or send an email to license@ebi-sib.ch).
CC -----
DR EMBL; AF027867; AAC97119.1; -.
DR REBASE; 1578; SacI.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
SQ SEQUENCE 358 AA; 39965 MW; EBF68CB8037EBF13 CRC64;

Query Match          91.4%; Score 32; DB 1; Length 358;
Best Local Similarity 83.3%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 347 ELDRWA 352

```

```

RESULT 32
NIAI_MAIZE
ID NIAI_MAIZE          STANDARD;          PRT;          621 AA.
AC P17571;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR) (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. W64 X W128E; TISSUE=Leaf;
RA Gowri G., Campbell W.H.;
RT "cDNA clones for corn leaf NADH: nitrate reductase and chloroplast
RT NAD(P) (+): glyceraldehyde-3-phosphate dehydrogenase.";
RL Plant Physiol. 90:792-798(1989).
RN [2]
RP REVISIONS TO 389-390; 405-406 AND 414-417, AND CHARACTERIZATION.
RC STRAIN=cv. W64 X W128E; TISSUE=Leaf;
RX MEDLINE=90267474; PubMed=2189408;
RA Hyde G.E., Campbell W.H.;
RT "High-level expression in Escherichia coli of the catalytically
RT active flavin domain of corn leaf NADH:nitrate reductase and its
RT comparison to human NADH:cytochrome b5 reductase.";
RL Biochem. Biophys. Res. Commun. 168:1285-1291(1990).
RN [3]
RP SECONDARY STRUCTURE OF FAD DOMAIN.
RX MEDLINE=92084635; PubMed=1748631;
RA Hyde G.E., Crawford N.M., Campbell W.H.;
RT "The sequence of squash NADH:nitrate reductase and its relationship
RT to the sequences of other flavoprotein oxidoreductases. A family of
RT flavoprotein pyridine nucleotide cytochrome b reductases.";
RL J. Biol. Chem. 266:23542-23547(1991).
RN [4]
RP MUTAGENESIS OF CYS-593.
RX MEDLINE=94245686; PubMed=8188655;
RA Dwivedi U.N., Shiraishi N., Campbell W.H.;
RT "Identification of an 'essential' cysteine of nitrate reductase via
RT mutagenesis of its recombinant cytochrome b reductase domain.";
RL J. Biol. Chem. 269:13785-13791(1994).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF FAD DOMAIN.
RX MEDLINE=95111952; PubMed=7812715;
RA Lu G., Campbell W.H., Schneider G., Lindqvist Y.;
RT "Crystal structure of the FAD-containing fragment of corn nitrate
RT reductase at 2.5-A resolution: relationship to other flavoprotein
RT reductases.";
RL Structure 2:809-821(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 232-501.
RX MEDLINE=95280311; PubMed=7760334;
RA Lu G., Lindqvist Y., Schneider G., Dwivedi U., Campbell W.H.;
RT "Structural studies on corn nitrate reductase: refined structure of
RT the cytochrome b reductase fragment at 2.5 A, its ADP complex and an
RT active-site mutant and modeling of the cytochrome b domain.";
RL J. Mol. Biol. 248:931-948(1995).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: Requires FAD, a heme group (called cytochrome b-557) and
CC one molybdenum atom.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----

```


FT DISULFID 388 452 BY SIMILARITY. (POTENTIAL).
 FT DISULFID 395 425 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 87 129 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 129 136 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 136 142 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 142 143 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 143 159 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 159 163 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 163 194 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 194 199 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 199 209 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 209 246 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 246 274 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 274 288 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 288 301 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 301 307 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 307 343 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 343 350 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 350 365 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 365 396 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 396 402 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 402 406 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 406 412 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 412 455 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 455 468 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 468 469 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 469 472 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 472 618 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 618 623 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 623 632 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 632 644 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 644 823 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 823 863 AA; 97743 MW; B729CB5A6FAD1641 CRC64;
 SQ SEQUENCE 863 AA; 97743 MW; B729CB5A6FAD1641 CRC64;
 Query Match 91.4%; Score 32; DB 1; Length 863;
 Best Local Similarity 83.3%; Pred. No. 83;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELDKWA 6
 DB 669 QLDKWA 674
 RESULT 34
 ENV_HV1C4
 ID ENV_HV1C4 STANDARD; PRT; 868 AA.
 AC P05879;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11687;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87041461; PubMed=3490666;
 RA Desai S.M., Kalyanaram V.S., Casey J.M., Srinivasan A.,
 RA Andersen P.R., Devare S.G.;
 RT "Molecular cloning and primary nucleotide sequence analysis of a
 RT distinct human immunodeficiency virus isolate reveal significant
 RT divergence in its genomic sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384 (1986).
 RN [2]
 RP SEQUENCE OF 34-43.
 RX MEDLINE=90253924; PubMed=2187500;
 RA Kalyanaram V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,
 RA DeVico A.L., Copeland T., Oroszian S., Gallo R.C., Sarngadharan M.G.;
 RT "Characterization of the secreted, native gp120 and gp160 of the human
 RT immunodeficiency virus type 1.";

RL AIDS Res. Hum. Retroviruses 6:371-380 (1990).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M13137; AAA44311.1; -;
 DR PIR; C25523; VCLJTH4.
 DR HIV; M13137; ENVSCD45.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 33
 FT CHAIN 34 522 EXTERIOR MEMBRANE GLYCOPROTEIN (GP120).
 FT CHAIN 523 868 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 55 75 BY SIMILARITY.
 FT DISULFID 120 216 BY SIMILARITY.
 FT DISULFID 127 207 BY SIMILARITY.
 FT DISULFID 132 163 BY SIMILARITY.
 FT DISULFID 229 258 BY SIMILARITY.
 FT DISULFID 239 250 BY SIMILARITY.
 FT DISULFID 307 341 BY SIMILARITY.
 FT DISULFID 387 456 BY SIMILARITY.
 FT DISULFID 394 429 BY SIMILARITY.
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 162 162 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 208 208 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 245 245 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 342 342 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 349 349 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 409 409 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 473 473 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 649 649 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 828 828 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 868 AA; 98698 MW; A11527FC52A6F0C8 CRC64;
 Query Match 91.4%; Score 32; DB 1; Length 868;
 Best Local Similarity 83.3%; Pred. No. 84;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELDKWA 6
 DB 674 QLDKWA 679

RESULT 35
NIA3_MAIZE
ID NIA3_MAIZE STANDARD; PRT; 889 AA.
AC P49102;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] 3 (EC 1.7.1.1) (NR).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73; TISSUE=Seedling;
RA Campbell W.H., Redinbaugh M.G., Ingemarsson B., Dougherty E.S.,
RA Campbell E.R.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD,
CC heme iron, and molybdenum-pterin as prosthetic groups. The heme
CC group is called cytochrome b-557 (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC

CC EMBL; U20450; AAA62316.1; -.
CC PIR; T02240; T02240.
CC HSSP; P17571; 2CND.
CC
CC MaizeDB; 30041; -.
CC InterPro; IPR001199; Cyt_B5.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR008335; Euk_Mb_oxred.
CC InterPro; IPR008333; FAD_binding_6.
CC InterPro; IPR001709; FPN_cyt_redctse.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR005066; Mo-co_dimer.
CC InterPro; IPR000572; Oxidored_molyb.
CC InterPro; IPR001433; Oxred_FAD/NAD(P).
CC InterPro; IPR001221; Phe_hydroxylase.
CC Pfam; PF009070; FAD_binding_6; 1.
CC Pfam; PF00173; heme_1; 1.
CC Pfam; PF03404; Mo-co_dimer; 1.
CC Pfam; PF00175; NAD_binding_1; 1.
CC Pfam; PF00174; oxidored_molyb; 1.
CC PRINTS; PR00406; CYTB5RDTASE.
CC PRINTS; PR00363; CYTOCHROME B5.
CC PRINTS; PR00407; EUMOPTERIN.
CC PRINTS; PR00371; FPNCR.
CC PRINTS; PR00410; PHEHYDRLASE.
CC ProDom; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME B5_1; 1.
CC PROSITE; PS00255; CYTOCHROME B5_2; 1.
CC PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation; Multigene family.
FT METAL 181 181
FT METAL 235 235
FT DISULFID 404 404
FT INTERCHAIN (POTENTIAL).
FT MOLYBDENUM-PTERIN (POTENTIAL).
FT MOLYBDENUM-PTERIN (POTENTIAL).
FT INTERCHAIN (POTENTIAL).

FT METAL 555 555 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 578 578 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 889 AA; 98811 MW; 3614A8BB44B822F5 CRC64;
Query Match 91.4%; Score 32; DB 1; Length 889;
Best Local Similarity 83.3%; Pred. No. 86;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
Db 806 ELDKWA 811
|||:|
|||:|
RESULT 36
NIA2_HORVU
ID NIA2_HORVU STANDARD; PRT; 912 AA.
AC P27959;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR) (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Steptoe; TISSUE=Leaf;
RX MEDLINE=91326031; PubMed=1865878;
RA Schnorr K.M., Juricek M., Huang C., Culley D., Kleinhofs A.;
RT "Analysis of barley nitrate reductase cDNA and genomic clones.";
RL Mol. Gen. Genet. 227:411-416(1991).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD,
CC heme iron, and molybdenum-pterin as prosthetic groups. The heme
CC group is called cytochrome b-557.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC

CC EMBL; X57844; CAA40975.1; -.
CC PIR; S17454; RDEHNS.
CC HSSP; P17571; 2CND.
CC InterPro; IPR001199; Cyt_B5.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR008335; Euk_Mb_oxred.
CC InterPro; IPR008333; FAD_binding_6.
CC InterPro; IPR001709; FPN_cyt_redctse.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR005066; Mo-co_dimer.
CC InterPro; IPR000572; Oxidored_molyb.
CC InterPro; IPR001433; Oxred_FAD/NAD(P).
CC Pfam; PF009070; FAD_binding_6; 1.
CC Pfam; PF00173; heme_1; 1.
CC Pfam; PF03404; Mo-co_dimer; 1.
CC Pfam; PF00175; NAD_binding_1; 1.
CC Pfam; PF00174; oxidored_molyb; 1.
CC PRINTS; PR00406; CYTB5RDTASE.
CC PRINTS; PR00363; CYTOCHROME B5.
CC PRINTS; PR00407; EUMOPTERIN.
CC PRINTS; PR00371; FPNCR.
CC PRINTS; PR00410; PHEHYDRLASE.
CC ProDom; PD000612; Cyt_B5; 1.
CC PROSITE; PS00191; CYTOCHROME B5_1; 1.
CC PROSITE; PS00255; CYTOCHROME B5_2; 1.
CC PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation; Multigene family.
FT METAL 181 181
FT METAL 235 235
FT DISULFID 404 404
FT INTERCHAIN (POTENTIAL).
FT MOLYBDENUM-PTERIN (POTENTIAL).
FT MOLYBDENUM-PTERIN (POTENTIAL).
FT INTERCHAIN (POTENTIAL).


```

DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PR0Dom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
DR OXidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation; Multigene family.
FT NON TER 1
FT METAL 186 186 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 240 240 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 425 425 INTERCHAIN (POTENTIAL).
FT METAL 570 570 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 593 593 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 912 AA; 101467 MW; 47AB9C5B303190CC CRC64;

Query Match 91.4%; Score 32; DB 1; Length 912;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 828 ELDRWA 833

RESULT 37
NIAL HORVU
ID NIAL HORVU STANDARD; PRT; 915 AA.
AC 27967;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Himalaya; TISSUE=Leaf;
RX MEDLINE=91326031; PubMed=1865878;
RA Schnorr K.M., Juricek M., Huang C., Culley D., Kleinhofs A.;
RT "Analysis of barley nitrate reductase cDNA and genomic clones.";
RL Mol. Genet. 227:411-416(1991).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD,
CC heme iron, and molybdenum-pterin as prosthetic groups. The heme
CC group is called cytochrome b-557.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X57845; CAA40976.1; -.
CC PIR; S17453; RDBHNH.
CC HSSP; P17571; 2CND.
CC InterPro; IPR001199; Cyt_B5.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR008335; Euk_Mb_oxred.
CC InterPro; IPR008333; FAD_binding_6.

```

```

DR InterPro; IPR001709; FPN_cyt_reductse.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR005066; Mo-co dimer.
DR InterPro; IPR000572; Oxidored_molyb.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF00173; heme_1; 1.
DR Pfam; PF03404; Mo-co dimer; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF00174; oxidored_molyb; 1.
DR PRINTS; PR00406; CYTB5RDTASE.
DR PRINTS; PR00363; CYTOCHROME B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PR0Dom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation; Multigene family.
FT METAL 189 189 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 243 243 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 428 428 INTERCHAIN (POTENTIAL).
FT METAL 573 573 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 596 596 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 915 AA; 101770 MW; 937FFA96B6FDA56 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 915;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 831 ELDRWA 836

RESULT 38
NIAL ORYSA
ID NIAL ORYSA STANDARD; PRT; 916 AA.
AC P16081;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR1).
GN NIAL.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartioideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M201;
RX MEDLINE=91370859; PubMed=2491689;
RA Cheng C., Dewdney J., Nam H., den Boer B.G.W., Goodman H.M.,
RA Choi H.K., Kleinhofs A., An G.;
RT "Nucleotide sequence of rice nitrate reductase genes.";
RL Plant Mol. Biol. 13:731-733(1989).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD,
CC heme iron, and molybdenum-pterin as prosthetic groups. The heme
CC group is called cytochrome b-557.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

CC	the European Bioinformatics Institute. There are no restrictions on its	RT	"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
CC	use by non-profit institutions as long as its content is in no way	RT	features of the regions of 4,504,864 bp covered by sixty P1 and TAC
CC	modified and this statement is not removed. Usage by and for commercial	RT	clones";
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/	RL	DNA Res. 7:131-135(2000).
CC	or send an email to license@isb-sib.ch).	CC	-I- FUNCTION: This magnesium-dependent enzyme catalyzes the hydrolysis
CC	-----	CC	of ATP coupled with the translocation of calcium from the cytosol
DR	EMBL; X15819; CAA33817.2; -	CC	out of the cell or into organelles (By similarity).
DR	EMBL; X15820; CAA33817.2; JOINED.	CC	-I- CATALYTIC ACTIVITY: ATP + H(2)O + Ca(2+) (Cis) = ADP + phosphate +
DR	PIR; S07554; S07554.	CC	Ca(2+) (Trans).
DR	HSSP; P17571; 2CND.	CC	-I- ENZYME REGULATION: Activated by calmodulin (By similarity).
DR	Gramene; P16081; -	CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.
DR	InterPro; IPR001199; Cyt B5.	CC	-I- DOMAIN: The N-terminus contains an autoinhibitory calmodulin-
DR	InterPro; IPR001834; Cyt_B5_reductase.	CC	binding domain, which binds calmodulin in a calcium-dependent
DR	InterPro; IPR008335; Euk_Mb_oxred.	CC	fashion (By similarity).
DR	InterPro; IPR008333; FAD_binding_6.	CC	-I- SIMILARITY: Belongs to the cation transport ATPases family (P-type
DR	InterPro; IPR001709; FEN_cyt_redctse.	CC	ATPases). Subfamily IIB.
DR	InterPro; IPR007110; Ig-like.	CC	-----
DR	InterPro; IPR005066; Mo-co_dimer.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
DR	InterPro; IPR000572; Oxidored_molylb.	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
DR	InterPro; IPR001433; Oxred_FAD/NAD(P).	CC	the European Bioinformatics Institute. There are no restrictions on its
DR	InterPro; IPR001221; Phe_hydroxylase.	CC	use by non-profit institutions as long as its content is in no way
DR	Pfam; PF00970; FAD_binding_6; 1.	CC	modified and this statement is not removed. Usage by and for commercial
DR	Pfam; PF00173; heme_1; 1.	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
DR	Pfam; PF03404; Mo-co_dimer; 1.	CC	or send an email to license@isb-sib.ch).
DR	Pfam; PF00175; NAD_binding_1; 1.	CC	-----
DR	Pfam; PF00174; oxidored_molylb; 1.	DR	EMBL; AB023045; BAB01709.1; -
DR	Pfam; PF00174; oxidored_molylb; 1.	DR	HSSP; P04191; 1EUL.
DR	PRINTS; PR00406; CYTB5RDTASE.	DR	InterPro; IPR006408; ATPase-IIB_Ca.
DR	PRINTS; PR00363; CYTOCHROME_B5.	DR	InterPro; IPR001757; ATPase_E1-E2.
DR	PRINTS; PR00407; EUMOPTERIN.	DR	InterPro; IPR006068; Cation_ATPase_C.
DR	PRINTS; PR00371; FPNCR.	DR	InterPro; IPR004014; Cation_ATPase_N.
DR	PRINTS; PR00410; PHEHYDRXILASE.	DR	InterPro; IPR008250; E1-E2_ATPase_reg.
DR	PRODOM; PR000612; Cyt_B5; 1.	DR	InterPro; IPR005834; Hydrolyase.
DR	PROSITE; PS00191; CYTOCHROME_B5_1; 1.	DR	InterPro; IPR00689; Cation_ATPase_C; 1.
DR	PROSITE; PS0255; CYTOCHROME_B5_2; 1.	DR	Pfam; PF00690; Cation_ATPase_N; 1.
DR	PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.	DR	Pfam; PF00122; E1-E2_ATPase; 1.
KW	Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;	DR	Pfam; PF00702; Hydrolyase; 1.
KW	Nitrate assimilation; Multigene family.	DR	PRINTS; PR00119; CATATPASE.
FT	METAL 192 192 MOLYBDENUM-PTERIN (POTENTIAL).	DR	TIGRFAMS; TIGR01517; ATPase-IIB_Ca; 1.
FT	METAL 246 246 MOLYBDENUM-PTERIN (POTENTIAL).	DR	TIGRFAMS; TIGR01494; ATPase_P-type; 5.
FT	DISULFID 431 431 INTERCHAIN (POTENTIAL).	DR	PROSITE; PS00154; ATPase_E1-E2; 1.
FT	METAL 576 576 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).	KW	Hydrolyase; Calcium transport; Transmembrane; Phosphorylation;
FT	METAL 599 599 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).	KW	ATP-binding; Metal-binding; Magnesium; Calmodulin-binding;
SQ	SEQUENCE 916 AA; 101482 MW; BB97DA33E1DEAEC9 CRC64;	KW	Multigene family; Hypothetical protein.
		FT	DOMAIN 1 181 CYTOPLASMIC (POTENTIAL).
		FT	TRANSMEM 182 202 POTENTIAL.
		FT	DOMAIN 203 220 LUMENAL (POTENTIAL).
		FT	TRANSMEM 221 241 POTENTIAL.
		FT	DOMAIN 242 369 CYTOPLASMIC (POTENTIAL).
		FT	TRANSMEM 370 389 POTENTIAL.
		FT	DOMAIN 390 426 LUMENAL (POTENTIAL).
		FT	TRANSMEM 427 444 POTENTIAL.
		FT	DOMAIN 445 844 CYTOPLASMIC (POTENTIAL).
		FT	TRANSMEM 845 863 POTENTIAL.
		FT	DOMAIN 864 874 LUMENAL (POTENTIAL).
		FT	TRANSMEM 875 895 POTENTIAL.
		FT	DOMAIN 896 915 CYTOPLASMIC (POTENTIAL).
		FT	TRANSMEM 916 938 POTENTIAL.
		FT	DOMAIN 939 950 LUMENAL (POTENTIAL).
		FT	TRANSMEM 951 975 POTENTIAL.
		FT	DOMAIN 976 993 CYTOPLASMIC (POTENTIAL).
		FT	TRANSMEM 994 1015 POTENTIAL.
		FT	DOMAIN 1016 1025 LUMENAL (POTENTIAL).
		FT	TRANSMEM 1026 1047 POTENTIAL.
		FT	DOMAIN 1048 1073 CYTOPLASMIC (POTENTIAL).
		FT	DOMAIN 44 55 CALMODULIN-BINDING (BY SIMILARITY).
		FT	MOD_RES 482 482 PHOSPHORYLATION (BY SIMILARITY).
		FT	METAL 789 789 MAGNESIUM (BY SIMILARITY).
		FT	METAL 793 793 MAGNESIUM (BY SIMILARITY).
		SQ	SEQUENCE 1073 AA; 117488 MW; 5AF6220EBD908069 CRC64;
			Query Match 91.4%; Score 32; DB 1; Length 1073;
			Best Local Similarity 83.3%; Pred. No. 1e+02;
			Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ELDKWA 6		
Db	832 ELDRWA 837		
RESULT 39			
ACA9 ARATH			
ID ACA9 ARATH	STANDARD; PRT; 1073 AA.		
AC Q9L041;			
DT 16-OCT-2001 (Rel. 40, Created)			
DT 16-OCT-2001 (Rel. 40, Last sequence update)			
DT 10-OCT-2003 (Rel. 42, Last annotation update)			
DE Potential calcium-transporting ATPase 9, plasma membrane-type			
DE (EC 3.6.3.8) (Ca(2+)-ATPase isoform 9).			
GN ACA9 OR AT3G21180 OR MXL8.3.			
OS Arabidopsis thaliana (Mouse-ear cress).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
OX NCBI_TaxID=3702;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=cv. Columbia;			
RX MEDLINE=20277480; PubMed=10819329;			
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;			

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
:|||||
Db 665 DLDKWA 670

RESULT 40

YAFU_ECOLI
ID YAFU_ECOLI STANDARD; PRT; 112 AA.
AC P77354;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yafu.
GN YAFU OR B0218.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]

SEQUENCE FROM N.A.

RP STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [2]

SEQUENCE FROM N.A.

RP Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,
RA Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
RA Lahekari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
RA Davis R.W.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL; AE000130; AAC73322.1; -;
DR EMBL; U70214; AAB08640.1; -;
DR PIR; C64746; C64746.
DR EcoGene; EG13333; yafu.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 22 42 POTENTIAL.
FT TRANSMEM 44 64 POTENTIAL.
SQ SEQUENCE 112 AA; 12136 MW; 7B8E901E02429F0D CRC64;

Query Match 88.6%; Score 31; DB 1; Length 112;

Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKW 5
:|||||
Db 90 ELDKW 94

RESULT 41

YAFI_SALTY
ID YAFI_SALTY STANDARD; PRT; 151 AA.
AC OXEM1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0178 protein yafi.

GN YAFI OR STM0397 OR STY0420 OR T2477.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2";
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18";
RL Nature 413:848-852(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyvanyi V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18";
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- SIMILARITY: Belongs to the UPF0178 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL; AE008713; AAL19341.1; -;
DR EMBL; AL627266; CAD08842.1; -;
DR EMBL; AE016842; AA070065.1; -;
DR styGene; SG77777; yafi.
DR HAMAP; MF 00489; -; 1.
DR InterPro; IPR003791; DUF188.
DR Pfam; PF02639; DUF188; 1.
DR ProDom; PD016319; DUF188; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 151 AA; 16945 MW; F94F40A401EA753B CRC64;

Query Match 88.6%; Score 31; DB 1; Length 151;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKW 5
:|||||
Db 139 ELDKW 143

RESULT 42

YU33 YERPE STANDARD; PRT; 152 AA.
AC Q8ZCF8; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DN Hypothetical UPF0178 protein YP03033/Y1450.
GN YP03033 OR Y1450.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagers K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RA "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RA "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
CC -1- SIMILARITY: Belongs to the UPF0178 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ414155; CAC92275.1; -;
DR EMBL; AE013748; AAM85021.1; -;
DR PIR; AH0368; AH0368.
DR HAMAP; MF 00489; -; 1.
DR InterPro; IPR003791; DUF188.
DR Pfam; PF02639; DUF188; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 152 AA; 17096 MW; E173AAF49D1BF176 CRC64;
Query Match 88.6%; Score 31; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKW 5
DB 139 ELDKW 143
RESULT 43
DHB2 MOUSE STANDARD; PRT; 381 AA.
AC P51658; O08898;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Estradiol 17 beta-dehydrogenase 2 (EC 1.1.1.62) (17-beta-HSD 2)
DE (17-beta-hydroxysteroid dehydrogenase 2).
GN

GN HSD17B2 OR EDH17B2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=973444259; PubMed=9224647;
RA Mustonen M.;
RT "Cloning of mouse 17beta-hydroxysteroid dehydrogenase type 2, and
RT analysing expression of the mRNAs for types 1, 2, 3, 4 and 5 in mouse
RT embryos and adult tissues.";
RL Biochem. J. 325:199-205(1997).
RN [2]
RP SEQUENCE OF 1-358 FROM N.A.
RC STRAIN=BALB/c;
RA Scofield W., Weiss B.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CAPABLE OF CATALYZING THE INTERCONVERSION OF
CC TESTOSTERONE AND ANDROSTENEDIONE, AS WELL AS ESTRADIOL AND
CC ESTRONE. ALSO HAS 20-ALPHA-HSD ACTIVITY. USES NADH WHILE EDH17B3
CC USES NADPH (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P) (+) = estrone +
CC NAD(P)H.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y09517; CAA70706.1; -;
DR EMBL; X95685; CAA64982.1; -;
DR HSP; P14061; IFDU.
DR MGI; MGI:1096386; Hsd17b2.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Steroid biosynthesis; Oxidoreductase; NAD; Multigene family;
KW Transmembrane; Signal-anchor
TRANSMEM 4 24 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT NP BIND 83 112 NAD (BY SIMILARITY).
FT ACT SITE 233 233 BY SIMILARITY.
FT CONFLICT 36 37 OA -> RP (IN REF. 2).
SQ SEQUENCE 381 AA; 41835 MW; 7AA62797947B6086 CRC64;
Query Match 88.6%; Score 31; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKW 5
DB 250 ELDKW 254
RESULT 44
GAG_HV1W2 STANDARD; PRT; 388 AA.
ID - GAG_HV1W2
AC P05689;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polypeptide [Contains: Core proteins P17, P24, P2, P7, P1, P6]
DE (Fragment).
GN

```

OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT at risk for AIDS.";
RL Science 232:1548-1553 (1986).
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- PTM: The p24 protein is phosphorylated.
CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K03457; AAB12988.1; -.
DR PDB; 1FGL; 01-APR-97.
DR HIV; K03457; GAG:WMJ2.
DR InterPro; IPR000721; Gag_p24.
DR InterPro; IPR008916; Retrov_capsid_C.
DR InterPro; IPR008919; Retrov_capsid_N.
DR InterPro; IPR000071; Retrov_p17.
DR Pfam; PF00540; Gag_p17; 1.
DR Pfam; PF00607; Gag_p24; 1.
DR PRINTS; PR00234; HIV1MATRIX.
KW AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
KW Zinc-finger; 3b-structure; Lipoprotein.
FT INIT MET 0 0 BY SIMILARITY.
FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
FT CHAIN 363 376 CORE PROTEIN P2.
FT CHAIN 377 >388 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
FT LIPID 1 1 N-myristoyl glycine (in host) (By
FT similarity).
FT NON TER 388 388
SQ SEQUENCE 388 AA; 43314 MW; EF895BE10ECF7804 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 388;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
Db 11 ELDKW 15

RESULT 45
GAL1_STRPN STANDARD; PRT; 392 AA.
AC Q97N26;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galactokinase (EC 2.7.1.6) (Galactose kinase).
GN GALK OR SP1853.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

```

```

OC Streptococcus.
OX NCBI_TaxID=13113;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Urkin A.S., White M., Kolonay J.F., Nelson M.C., Peterson J.D.,
RA Unayam L.A., Gwin O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Usterback T.R., Hansen C.L.,
RA McDonald L.E., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollinghead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506 (2001).
CC -1- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
CC phosphate.
CC -1- PATHWAY: Galactose metabolism; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -1- SIMILARITY: Belongs to the GHMP kinase family. GALK subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE007477; AAK75925.1; -.
DR PIR; D95216; D95216.
DR TIGR; SP1853; -.
DR HAMAP; MF_00246; -.
DR InterPro; IPR000705; Galactokinase.
DR InterPro; IPR006204; GHMP kinase.
DR InterPro; IPR006203; GHMPKns_ATP.
DR InterPro; IPR006206; Mv_Galkinase.
DR Pfam; PF00288; GHMP kinases; 1.
DR PRINTS; PR00473; GALKTOKINASE.
DR PRINTS; PR00959; MEVGALKINASE.
DR TIGRFAMs; TIGR00131; gal_kin; 1.
DR PROSITE; PS00106; GALKTOKINASE; 1.
DR PROSITE; PS00627; GHMP KINASES ATP; 1.
KW Transferase; Kinase; Galactose metabolism; ATP-binding;
KW Complete proteome.
FT NP BIND 126 136 ATP (POTENTIAL).
FT NP BIND 126 136 ATP (POTENTIAL).
SQ SEQUENCE 392 AA; 43584 MW; 946034F1FEA50095 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 392;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
Db 253 ELDEWA 258

RESULT 46
GAL1_STRRG STANDARD; PRT; 392 AA.
ID GAL1_STRRG
AC Q8DNK7;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Galactokinase (EC 2.7.1.6) (Galactose kinase).
GN GALK OR SP1668.
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]

```

SEQUENCE FROM N.A.
RX MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.B. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rokey P.,
RA Sun P.-M., Winkler M.B., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
CC -1- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
CC phosphate.
CC -1- PATHWAY: Galactose metabolism; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the GHMP kinase family. Galk subfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AE008532; ALU00471.1; -.
DR PIR; B98080; B98080.
DR HAMAP; MF 00246; -; 1.
DR InterPro; IPR000705; Galactokinase.
DR InterPro; IPR006203; GHMPkinase ATP.
DR InterPro; IPR006204; GHMP kinase.
DR InterPro; IPR006206; Mv_galkinase.
DR Pfam; PF00288; GHMP kinases; 1.
DR PRINTS; PR00473; GALCTOKINASE.
DR PRINTS; PR00959; MEVGALKINASE.
DR TIGRFAMS; TIGR00131; gal kin; 1.
DR PROSITE; PS00106; GALACTOKINASE; 1.
DR PROSITE; PS00627; GHMP_KINASE_ATP; 1.
KW Transferase; Kinase; Galactose metabolism; ATP-binding;
KW Complete proteome.
FT NP BIND 126 136 ATP (POTENTIAL).
SQ SEQUENCE 392 AA; 43672 MW; 8503611AC5FCC394 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 392;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
DB 253 ELDEWA 258
|||||

RESULT 47
ECB2_HALEL STANDARD; PRT; 421 AA.
ID ECB2_HALEL
AC OS2250;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Diaminobutyrate-pyruvate aminotransferase (EC 2.6.1.46) (L-
DE diaminobutyric acid transaminase) (Diaminobutyrate transaminase).
GN ECTB.
OS Halomonas elongata.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC Halomonadaceae; Halomonas.
OC NCBI_TaxID=2746;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 2581T.
RX MEDLINE=98231640; PubMed=9570121;
RA Goller K., Ofer A., Galinski E.A.;

"Construction and characterization of an NaCl-sensitive mutant of
RT Halomonas elongata impaired in ectoine biosynthesis.";
RL FEMS Microbiol. Lett. 161:293-300(1998).
CC -1- CATALYTIC ACTIVITY: L-2,4-diaminobutanoate + pyruvate = L-
CC aspartate 4-semialdehyde + L-alanine.
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- PATHWAY: Biosynthesis of ectoine (1,4,5,6-tetrahydro-2-methyl-4-
CC pyrimidine carboxylic acid); first step.
CC -1- SUBUNIT: Homohexamer (By similarity).
CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF031489; AAC15882.1; -.
DR HSP; P12995; LQJ3.
DR InterPro; IPR005814; Aminotrans_3.
DR InterPro; IPR004637; Dat..
DR Pfam; PF00202; aminotran_3; 1.
DR TIGRFAMS; TIGR00709; dat; 1.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; FALSE NEG.
KW Transferase; Aminotransferase; Pyridoxal phosphate.
FT BINDING 267 267 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 421 AA; 46166 MW; A4A2E21596E1E16C CRC64;

Query Match 88.6%; Score 31; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
DB 284 ELDKW 288
|||||

RESULT 48
GAG_HVIOY STANDARD; PRT; 498 AA.
ID GAG_HVIOY
AC P20889;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polypeptide [Contains: Core proteins P17, P24, P2, P7, P1, P6].
GN GAG.
OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11699;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90148544; PubMed=2559749;
RA Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.;
RT "A highly defective HIV-1 strain isolated from a healthy Gabonese
RT individual presenting an atypical western blot.";
RL AIDS 3:707-715(1989)
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- PTM: The p24 protein is phosphorylated.
CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
CC HEALTHY GABONESE INDIVIDUAL.
CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; M26727; AAA83391.1; -
HSPF; P05888; IAAP.
HIV; M26727; GAGSOYI.
InterPro; IPR000721; Gag_p24.
InterPro; IPR008916; Retrov capsid C.
InterPro; IPR008919; Retrov capsid N.
InterPro; IPR000071; Retrov p17.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00098; Zf_CCHC; 2.
PRINTS; PR00939; C2HCZNFINGER.
SMART; SM00343; HIVM1MATRIX.
PROSITE; PS0158; ZF_CCHC; 2.
AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
Zinc-finger; Repeat; Lipoprotein.
INIT MET 0 BY SIMILARITY.
CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
CHAIN 363 376 CORE PROTEIN P2.
CHAIN 377 430 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
CHAIN 431 446 CORE PROTEIN P1.
CHAIN 447 498 CORE PROTEIN P6.
ZN_FING 388 405 CCHC-TYPE 1.
ZN_FING 409 426 CCHC-TYPE 2.
LIPID 1 1 N-myristoyl glycine (in host) (By similarity).
SEQUENCE 498 AA; 55451 MW; BDFP20658DEB20B1 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKW 5
Db 11 ELDKW 15

RESULT 49
GAG_HV1N5
ID - GAG_HV1N5 STANDARD; PRT; 499 AA.
AC P12493;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polyprotein [Contains: Core proteins P17, P24, P2, P7, P1, P6].
GN GAG.
OS Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11698;
RN [1]
RP SEQUENCE FROM N.A. (CLONE PNL4-3).
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RL Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- PTM: The p24 protein is phosphorylated.
CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; M19921; AAA44987.1; -
PDB; 1A43; 09-FEB-99.
PDB; 1A80; 28-OCT-98.
PDB; 1AFV; 20-AUG-97.
PDB; 1AK4; 15-OCT-97.
PDB; 1AUM; 14-JAN-98.
PDB; 1BAJ; 18-NOV-98.
PDB; 1GDS; 30-DEC-96.
PDB; 1GDI; 30-DEC-96.
PDB; 1GDZ; 30-DEC-96.
PDB; 1GWP; 21-JUN-02.
HIV; M19921; GAGSL43.
InterPro; IPR000721; Gag_p24.
InterPro; IPR008916; Retrov capsid C.
InterPro; IPR008919; Retrov capsid N.
InterPro; IPR000071; Retrov p17.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00098; Zf_CCHC; 2.
PRINTS; PR00939; C2HCZNFINGER.
SMART; SM00343; HIVM1MATRIX.
PROSITE; PS0158; ZF_CCHC; 2.
AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
Zinc-finger; Repeat; 3D-structure; Lipoprotein.
INIT MET 0 BY SIMILARITY.
CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
CHAIN 363 376 CORE PROTEIN P2.
CHAIN 377 431 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
CHAIN 432 447 CORE PROTEIN P1.
CHAIN 448 499 CORE PROTEIN P6.
ZN_FING 389 406 CCHC-TYPE 1.
ZN_FING 410 427 CCHC-TYPE 2.
LIPID 1 1 N-myristoyl glycine (in host) (By similarity).
SEQUENCE 499 AA; 55687 MW; C8ECC1302FE2C1E2 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKW 5
Db 11 ELDKW 15

RESULT 50
GAG_HV1Y2
ID - GAG_HV1Y2 STANDARD; PRT; 499 AA.
AC P35962;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polyprotein [Contains: Core proteins P17, P24, P2, P7, P1, P6].
GN GAG.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=36377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93021387; PubMed=1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
RA Shaw G.M.;
RT "Complete nucleotide sequence, genome organization, and biological properties of human immunodeficiency virus type 1 in vivo: evidence

```

RT for limited defectiveness and complementation."
RL J. Virol. 66:6587-6600(1992).
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- PTM: The p24 protein is phosphorylated.
CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M93258; -; NOT_ANNOTATED_CDS.
CC PIR; A44001; A44001.
CC PDB; IF6U; 09-OCT-00.
CC PDB; IMFS; 17-JUN-98.
CC InterPro; IPR000721; Gag_p24.
CC InterPro; IPR008916; Retrov capsid C.
CC InterPro; IPR008919; Retrov capsid_N.
CC InterPro; IPR000071; Retrovir_P17.
CC InterPro; IPR001878; Znf_CCHC.
CC Pfam; PF00540; Gag_P17; 1.
CC Pfam; PF00607; Gag_P24; 1.
CC Pfam; PF00098; zf-CCHC; 2.
CC PRINTS; PR00939; C2HCZNFINGER.
CC PRINTS; PR00234; HIVMATRIX.
CC SMART; SM00343; Znf_C2HC; 2.
CC PROSITE; PS50158; ZF_CCHC; 2.
KW AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
KW Zinc-finger; Repeat; 3D-structure; Lipoprotein.
FT INIT MET 0 0 BY SIMILARITY.
FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
FT CHAIN 363 376 CORE PROTEIN P2.
FT CHAIN 377 431 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
FT CHAIN 432 447 CORE PROTEIN P1.
FT CHAIN 448 499 CORE PROTEIN P6.
FT CHAIN 389 406 CCHC-TYPE 1.
FT ZN_FING 410 427 CCHC-TYPE 2.
FT ZN_FING 1 1 N-myristoyl glycine (in host) (By
FT LIPID 1 1 similarity).
FT -----
SQ SEQUENCE 499 AA; 55660 MW; 278E665F5405CD99 CRC64;
Query Match 88.6%; Score 31; DB 1; Length 499;
Best Local Similarity 100.0%; Pred.No.75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ELDKW 5
Db 11 ELDKW 15

```

Search completed: March 16, 2004, 09:16:51
Job time : 18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2004, 09:11:00 ; Search time 39 Seconds
(without alignments)
48.541 Million cell updates/sec

Title: US-10-024-329-2

Perfect score: 35

Sequence: 1 ELDRWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

SPTREMBL 25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	34	15	Q69904 human immun
2	35	100.0	34	15	Q69905 human immun
3	35	100.0	34	15	Q69893 human immun
4	35	100.0	34	15	Q69903 human immun
5	35	100.0	34	15	Q69894 human immun
6	35	100.0	41	15	Q69891 human immun
7	35	100.0	41	15	Q69892 human immun
8	35	100.0	42	15	Q69910 human immun
9	35	100.0	49	15	Q69896 human immun
10	35	100.0	49	15	Q69906 human immun
11	35	100.0	49	15	Q69907 human immun
12	35	100.0	49	15	Q69895 human immun
13	35	100.0	49	15	Q69909 human immun
14	35	100.0	50	15	Q69898 human immun
15	35	100.0	57	15	Q69913 human immun
16	35	100.0	57	15	Q69912 human immun

17	35	100.0	57	15	Q69911 human immun
18	35	100.0	117	15	Q9QGN5 human immun
19	35	100.0	117	15	Q9YRS9 human immun
20	35	100.0	117	15	Q9YVW7 human immun
21	35	100.0	117	15	Q9YRS2 human immun
22	35	100.0	117	15	Q9YVW1 human immun
23	35	100.0	118	15	Q9ESR1 human immun
24	35	100.0	118	15	Q9ESG3 human immun
25	35	100.0	118	15	Q9ESG2 human immun
26	35	100.0	118	15	Q9Y202 human immun
27	35	100.0	122	15	Q9EA94 human immun
28	35	100.0	122	15	Q9YXN9 human immun
29	35	100.0	122	15	Q9EA85 human immun
30	35	100.0	122	15	Q9EA81 human immun
31	35	100.0	122	15	Q9YXQ0 human immun
32	35	100.0	122	15	Q9QIW4 human immun
33	35	100.0	122	15	Q9EA44 human immun
34	35	100.0	122	15	Q9QIW0 human immun
35	35	100.0	122	15	Q9IUN1 human immun
36	35	100.0	122	15	Q9WQZ0 human immun
37	35	100.0	122	15	Q9YXR6 human immun
38	35	100.0	122	15	Q9QIU3 human immun
39	35	100.0	122	15	Q9EA45 human immun
40	35	100.0	122	15	Q9IUM8 human immun
41	35	100.0	122	15	Q9EAA2 human immun
42	35	100.0	122	15	Q9QX77 human immun
43	35	100.0	122	15	Q9WQZ1 human immun
44	35	100.0	122	15	Q9EA99 human immun
45	35	100.0	122	15	Q9YXR8 human immun
46	35	100.0	122	15	Q9IUN5 human immun
47	35	100.0	122	15	Q9WQY8 human immun
48	35	100.0	122	15	Q9IQQ0 human immun
49	35	100.0	122	15	Q9YXP7 human immun
50	35	100.0	122	15	Q9WQZ7 human immun
51	35	100.0	122	15	Q9IUN9 human immun
52	35	100.0	122	15	Q9YXN9 human immun
53	35	100.0	122	15	Q9EA90 human immun
54	35	100.0	122	15	Q9YXN4 human immun
55	35	100.0	122	15	Q9QIW9 human immun
56	35	100.0	122	15	Q9QIW7 human immun
57	35	100.0	122	15	Q9EA84 human immun
58	35	100.0	122	15	Q9IUP8 human immun
59	35	100.0	122	15	Q9WQY9 human immun
60	35	100.0	122	15	Q9YXR0 human immun
61	35	100.0	122	15	Q9EA97 human immun
62	35	100.0	122	15	Q9YXP1 human immun
63	35	100.0	122	15	Q9QIV0 human immun
64	35	100.0	122	15	Q9YXR4 human immun
65	35	100.0	122	15	Q9YXQ1 human immun
66	35	100.0	122	15	Q9QX88 human immun
67	35	100.0	122	15	Q9EA93 human immun
68	35	100.0	122	15	Q9YXQ8 human immun
69	35	100.0	122	15	Q9YXR1 human immun
70	35	100.0	122	15	Q9QIV1 human immun
71	35	100.0	122	15	Q9YXR2 human immun
72	35	100.0	122	15	Q9QIW2 human immun
73	35	100.0	122	15	Q9EA89 human immun
74	35	100.0	122	15	Q9YXN0 human immun
75	35	100.0	122	15	Q9IQQ3 human immun
76	35	100.0	122	15	Q9QIW5 human immun
77	35	100.0	122	15	Q9QIV4 human immun
78	35	100.0	122	15	Q9YXR7 human immun
79	35	100.0	122	15	Q9IUN6 human immun
80	35	100.0	122	15	Q9QX20 human immun
81	35	100.0	122	15	Q9IQQ6 human immun
82	35	100.0	122	15	Q9IUN3 human immun
83	35	100.0	122	15	Q9YXP2 human immun
84	35	100.0	122	15	Q9IJP2 human immun
85	35	100.0	122	15	Q9YXN1 human immun
86	35	100.0	122	15	Q9IQQ1 human immun
87	35	100.0	122	15	Q9EA80 human immun
88	35	100.0	122	15	Q9IQQ9 human immun
89	35	100.0	122	15	Q9IQR0 human immun

90	35	100.0	122	15	Q9EA92	Q9ea92	human	immun	163	35	100.0	144	15	Q7ZCC1	Q7zcc1	human	immun
91	35	100.0	122	15	Q9YXP4	Q9yxp4	human	immun	164	35	100.0	144	15	Q7ZCB9	Q7zcb9	human	immun
92	35	100.0	122	15	Q9IUQ2	Q9iuiq2	human	immun	165	35	100.0	144	15	Q7ZCB8	Q7zcb8	human	immun
93	35	100.0	122	15	Q9EA82	Q9ea82	human	immun	166	35	100.0	144	15	Q7ZCB7	Q7zcb7	human	immun
94	35	100.0	122	15	Q9IJP1	Q9iip1	human	immun	167	35	100.0	144	15	Q7ZCB6	Q7zcb6	human	immun
95	35	100.0	122	15	Q90DJ7	Q90dj7	human	immun	168	35	100.0	144	15	Q7ZCB5	Q7zcb5	human	immun
96	35	100.0	122	15	Q90DL6	Q90dl6	human	immun	169	35	100.0	144	15	Q7ZCB4	Q7zcb4	human	immun
97	35	100.0	122	15	Q9WR00	Q9wr00	human	immun	170	35	100.0	144	15	Q7ZCB3	Q7zcb3	human	immun
98	35	100.0	122	15	Q9YXN5	Q9yxns	human	immun	171	35	100.0	144	15	Q7ZCB2	Q7zcb2	human	immun
99	35	100.0	122	15	Q9QIU8	Q9qiu8	human	immun	172	35	100.0	144	15	Q7ZCB1	Q7zcb1	human	immun
100	35	100.0	122	15	Q9YXP0	Q9yxp0	human	immun	173	35	100.0	144	15	Q7ZCB0	Q7zcb0	human	immun
101	35	100.0	122	15	Q9YXQ2	Q9yxq2	human	immun	174	35	100.0	144	15	Q7ZCA9	Q7zca9	human	immun
102	35	100.0	122	15	Q9IJP7	Q9iip7	human	immun	175	35	100.0	144	15	Q7ZCA4	Q7zca4	human	immun
103	35	100.0	122	15	Q9IJP3	Q9iip3	human	immun	176	35	100.0	144	15	Q7ZCA3	Q7zca3	human	immun
104	35	100.0	122	15	Q7ZJ90	Q7zj90	human	immun	177	35	100.0	144	15	Q7ZCA2	Q7zca2	human	immun
105	35	100.0	122	15	Q7ZJR9	Q7zjr9	human	immun	178	35	100.0	144	15	Q7ZCA1	Q7zca1	human	immun
106	35	100.0	122	15	Q7ZJR8	Q7zjr8	human	immun	179	35	100.0	144	15	Q7ZCA0	Q7zca0	human	immun
107	35	100.0	122	15	Q7ZJR7	Q7zjr7	human	immun	180	35	100.0	144	15	Q7ZC99	Q7zcc99	human	immun
108	35	100.0	122	15	Q7ZJR6	Q7zjr6	human	immun	181	35	100.0	144	15	Q7ZC96	Q7zcc96	human	immun
109	35	100.0	122	15	Q7ZJR5	Q7zjr5	human	immun	182	35	100.0	144	15	Q7ZC95	Q7zcc95	human	immun
110	35	100.0	122	15	Q7ZJR4	Q7zjr4	human	immun	183	35	100.0	144	15	Q7ZC94	Q7zcc94	human	immun
111	35	100.0	122	15	Q7ZJQ3	Q7zjq3	human	immun	184	35	100.0	144	15	Q7ZC93	Q7zcc93	human	immun
112	35	100.0	122	15	Q7ZJQ2	Q7zjq2	human	immun	185	35	100.0	144	15	Q7ZC91	Q7zcc91	human	immun
113	35	100.0	122	15	Q7ZJQ1	Q7zjq1	human	immun	186	35	100.0	144	15	Q7ZC89	Q7zcc89	human	immun
114	35	100.0	122	15	Q7ZJQ0	Q7zjq0	human	immun	187	35	100.0	144	15	Q7ZC88	Q7zcc88	human	immun
115	35	100.0	122	15	Q7ZJP9	Q7zjp9	human	immun	188	35	100.0	144	15	Q7ZC87	Q7zcc87	human	immun
116	35	100.0	122	15	Q7ZJP8	Q7zjp8	human	immun	189	35	100.0	144	15	Q7ZC86	Q7zcc86	human	immun
117	35	100.0	122	15	Q7ZJP7	Q7zjp7	human	immun	190	35	100.0	144	15	Q7ZC85	Q7zcc85	human	immun
118	35	100.0	122	15	Q7ZJP6	Q7zjp6	human	immun	191	35	100.0	144	15	Q7ZC84	Q7zcc84	human	immun
119	35	100.0	122	15	Q8J3S3	Q8j3s3	human	immun	192	35	100.0	144	15	Q7ZC74	Q7zcc74	human	immun
120	35	100.0	123	15	Q8UME5	Q8umes	human	immun	193	35	100.0	144	15	Q7ZC73	Q7zcc73	human	immun
121	35	100.0	123	15	Q9EAA3	Q9eaa3	human	immun	194	35	100.0	144	15	Q7ZC71	Q7zcc71	human	immun
122	35	100.0	123	15	Q9YXR3	Q9yxr3	human	immun	195	35	100.0	144	15	Q7ZC70	Q7zcc70	human	immun
123	35	100.0	123	15	Q8AEX5	Q8aex5	human	immun	196	35	100.0	144	15	Q7ZC45	Q7zcc45	human	immun
124	35	100.0	123	15	Q8AEX4	Q8aex4	human	immun	197	35	100.0	145	15	Q7ZC57	Q7zcc57	human	immun
125	35	100.0	123	15	Q8AEX2	Q8aex2	human	immun	198	35	100.0	145	15	Q7ZC55	Q7zcc55	human	immun
126	35	100.0	123	15	Q8AEX1	Q8aex1	human	immun	199	35	100.0	145	15	Q7ZC54	Q7zcc54	human	immun
127	35	100.0	124	15	Q8J3R7	Q8j3r7	human	immun	200	35	100.0	145	15	Q7SM37	Q7sm37	human	immun
128	35	100.0	127	11	Q9D4Q2	Q9d4q2	mus	musculus	201	35	100.0	146	15	Q7SLY9	Q7sly9	human	immun
129	35	100.0	127	15	Q9YXQ0	Q9yxx0	human	immun	202	35	100.0	147	15	Q8JM03	Q8jm03	human	immun
130	35	100.0	127	15	Q9YZ16	Q9yz16	human	immun	203	35	100.0	153	15	Q8J3P4	Q8j3p4	human	immun
131	35	100.0	129	15	Q9YV25	Q9yv25	human	immun	204	35	100.0	155	15	Q8J3P8	Q8j3p8	human	immun
132	35	100.0	130	15	Q90Q14	Q90q14	human	immun	205	35	100.0	155	15	Q8J3P6	Q8j3p6	human	immun
133	35	100.0	132	15	Q90Q52	Q90q52	human	immun	206	35	100.0	155	15	Q8J3P5	Q8j3p5	human	immun
134	35	100.0	132	15	Q90Q52	Q90q52	human	immun	207	35	100.0	155	15	Q8J3N5	Q8j3n5	human	immun
135	35	100.0	132	15	Q91WQ5	Q91wq5	human	immun	208	35	100.0	155	15	Q8J3N2	Q8j3n2	human	immun
136	35	100.0	132	15	Q7SLZ2	Q7slz2	human	immun	209	35	100.0	155	15	Q8J3N1	Q8j3n1	human	immun
137	35	100.0	133	15	Q90Q30	Q90q30	human	immun	210	35	100.0	155	15	Q8J3N0	Q8j3n0	human	immun
138	35	100.0	133	15	Q90Q57	Q90q57	human	immun	211	35	100.0	159	15	Q8JER6	Q8jer6	human	immun
139	35	100.0	133	15	Q90Q63	Q90q63	human	immun	212	35	100.0	161	15	Q8JER1	Q8jer1	human	immun
140	35	100.0	133	15	Q90Q53	Q90q53	human	immun	213	35	100.0	163	15	Q90E80	Q90e80	human	immun
141	35	100.0	133	15	Q90Q20	Q90q20	human	immun	214	35	100.0	163	15	Q90E69	Q90e69	human	immun
142	35	100.0	138	15	Q7SLZ3	Q7slz3	human	immun	215	35	100.0	163	15	Q90E77	Q90e77	human	immun
143	35	100.0	139	15	Q7SLZ9	Q7slz9	human	immun	216	35	100.0	163	15	Q90E68	Q90e68	human	immun
144	35	100.0	142	15	Q7ZC67	Q7zcc67	human	immun	217	35	100.0	163	15	Q90E63	Q90e63	human	immun
145	35	100.0	143	15	Q7ZC46	Q7zcc46	human	immun	218	35	100.0	163	15	Q90E79	Q90e79	human	immun
146	35	100.0	143	15	Q7SM06	Q7sm06	human	immun	219	35	100.0	163	15	Q90E61	Q90e61	human	immun
147	35	100.0	144	15	Q7ZCF1	Q7zcf1	human	immun	220	35	100.0	163	15	Q90E71	Q90e71	human	immun
148	35	100.0	144	15	Q7ZCF0	Q7zcf0	human	immun	221	35	100.0	163	15	Q90E74	Q90e74	human	immun
149	35	100.0	144	15	Q7ZCE8	Q7zce8	human	immun	222	35	100.0	163	15	Q90E75	Q90e75	human	immun
150	35	100.0	144	15	Q7ZCE4	Q7zce4	human	immun	223	35	100.0	163	15	Q90E72	Q90e72	human	immun
151	35	100.0	144	15	Q7ZCE3	Q7zce3	human	immun	224	35	100.0	163	15	Q90E60	Q90e60	human	immun
152	35	100.0	144	15	Q7ZCE2	Q7zce2	human	immun	225	35	100.0	163	15	Q90E56	Q90e56	human	immun
153	35	100.0	144	15	Q7ZCE1	Q7zce1	human	immun	226	35	100.0	163	15	Q90E66	Q90e66	human	immun
154	35	100.0	144	15	Q7ZCD8	Q7zcd8	human	immun	227	35	100.0	163	15	Q90E78	Q90e78	human	immun
155	35	100.0	144	15	Q7ZCD7	Q7zcd7	human	immun	228	35	100.0	164	15	Q90E81	Q90e81	human	immun
156	35	100.0	144	15	Q7ZCD6	Q7zcd6	human	immun	229	35	100.0	164	15	Q8JER5	Q8jer5	human	immun
157	35	100.0	144	15	Q7ZCD3	Q7zcd3	human	immun	230	35	100.0	164	15	Q90E64	Q90e64	human	immun
158	35	100.0	144	15	Q7ZCD2	Q7zcd2	human	immun	231	35	100.0	164	15	Q90E70	Q90e70	human	immun
159	35	100.0	144	15	Q7ZCD1	Q7zcd1	human	immun	232	35	100.0	164	15	Q90E82	Q90e82	human	immun
160	35	100.0	144	15	Q7ZCC9	Q7zcc9	human	immun	233	35	100.0	164	15	Q8JER2	Q8jer2	human	immun
161	35	100.0	144	15	Q7ZCC9	Q7zcc9	human	immun	234	35	100.0	167	15	Q8JAM3	Q8jam3	human	immun
162	35	100.0	144	15	Q7ZCC2	Q7zcc2	human	immun	235	35	100.0	168	15	Q8JAM3	Q8jam3	human	immun

236	35	100.0	169	15	08JER0	08jer0 human immun	309	35	100.0	830	15	07SUQ2	Q7suq2 human immun
237	35	100.0	169	15	08JER0	Q8jed9 human immun	310	35	100.0	833	15	09QK14	Q9qk14 human immun
238	35	100.0	173	15	08JAU9	Q8ja9 human immun	311	35	100.0	833	15	09QKH9	Q9qkh9 human immun
239	35	100.0	178	15	08JAM4	Q8jam4 human immun	312	35	100.0	833	15	09QKI3	Q9qki3 human immun
240	35	100.0	179	15	08JAK7	Q8jak7 human immun	313	35	100.0	835	15	09QVF1	Q9qvf1 human immun
241	35	100.0	190	15	08JAL7	Q8jal7 human immun	314	35	100.0	835	15	076074	Q76074 human immun
242	35	100.0	192	15	08JAL2	Q8jal2 human immun	315	35	100.0	837	15	09QKJ6	Q9qkj6 human immun
243	35	100.0	195	15	08JAY4	Q8jay4 human immun	316	35	100.0	837	15	09QKJ5	Q9qkj5 human immun
244	35	100.0	199	15	08JAL3	Q8jal3 human immun	317	35	100.0	838	15	09QKJ5	Q9qkj5 human immun
245	35	100.0	201	15	08JAL6	Q8jal6 human immun	318	35	100.0	839	15	073364	Q73364 human immun
246	35	100.0	201	15	08JAL5	Q8jal5 human immun	319	35	100.0	840	15	070694	Q70694 human immun
247	35	100.0	201	15	08JAL8	Q8jal8 human immun	320	35	100.0	841	15	09E1S4	Q9e1s4 human immun
248	35	100.0	202	15	08JAK5	Q8jak5 human immun	321	35	100.0	841	15	09QKJ1	Q9qkj1 human immun
249	35	100.0	218	15	08JAK5	Q8jak5 human immun	322	35	100.0	841	15	041556	Q41556 human immun
250	35	100.0	219	15	08JAU4	Q8ja4 human immun	323	35	100.0	842	15	08JBQ5	Q8jbq5 human immun
251	35	100.0	246	15	08JF92	Q8jf92 human immun	324	35	100.0	843	15	041610	Q41610 human immun
252	35	100.0	264	11	09CPY3	Q9cpy3 mus musculus	325	35	100.0	843	15	070150	Q70150 human immun
253	35	100.0	307	4	Q8BVW3	Q8bv3 homo sapien	326	35	100.0	843	15	09QKH8	Q9qkh8 human immun
254	35	100.0	323	11	08ROF7	Q8rof7 mus musculus	327	35	100.0	843	15	070008	Q70008 human immun
255	35	100.0	357	15	078118	Q78118 human immun	328	35	100.0	844	15	056561	Q56561 human immun
256	35	100.0	357	15	078119	Q78119 human immun	329	35	100.0	845	15	08UNF5	Q8unf5 human immun
257	35	100.0	357	15	078112	Q78112 human immun	330	35	100.0	845	15	070679	Q70679 human immun
258	35	100.0	358	15	078120	Q78120 human immun	331	35	100.0	845	15	09QR81	Q9qrb1 human immun
259	35	100.0	443	15	080023	Q80023 human immun	332	35	100.0	845	15	07SV04	Q7sv04 human immun
260	35	100.0	445	15	080021	Q80021 human immun	333	35	100.0	845	15	07SPQ3	Q7spq3 human immun
261	35	100.0	465	11	09CXF0	Q9cxf0 mus musculus	334	35	100.0	846	15	08UL63	Q8ul63 human immun
262	35	100.0	616	15	0993B0	Q993b0 human immun	335	35	100.0	846	15	056111	Q56111 human immun
263	35	100.0	618	15	0993B0	Q993b2 human immun	336	35	100.0	846	15	09PXW7	Q9pxw7 human immun
264	35	100.0	635	15	090U82	Q90u82 human immun	337	35	100.0	847	15	041537	Q41537 human immun
265	35	100.0	645	15	0993A6	Q993a6 human immun	338	35	100.0	847	15	090DU1	Q90du1 human immun
266	35	100.0	668	15	091JZ3	Q91jz3 human immun	339	35	100.0	847	15	069996	Q69996 human immun
267	35	100.0	679	15	09JOG5	Q9jog5 human immun	340	35	100.0	847	15	075760	Q75760 human immun
268	35	100.0	684	15	09IK06	Q9ik06 human immun	341	35	100.0	847	15	076125	Q76125 human immun
269	35	100.0	698	10	09XHV2	Q9xhv2 oryza sativ	342	35	100.0	847	15	08Q366	Q8q366 human immun
270	35	100.0	724	15	09QKH4	Q9qkh4 human immun	343	35	100.0	847	15	08A821	Q8ar21 human immun
271	35	100.0	727	15	09Q723	Q9q723 human immun	344	35	100.0	847	15	07ZB20	Q7zb20 human immun
272	35	100.0	727	15	09QKJ3	Q9qkj3 human immun	345	35	100.0	848	15	074999	Q74999 human immun
273	35	100.0	732	15	09QKJ2	Q9qkj2 human immun	346	35	100.0	848	15	069988	Q69988 human immun
274	35	100.0	747	15	070607	Q70607 human immun	347	35	100.0	848	15	09E1S3	Q9e1s3 human immun
275	35	100.0	748	15	070606	Q70606 human immun	348	35	100.0	848	15	076123	Q76123 human immun
276	35	100.0	748	15	08J582	Q8j582 human immun	349	35	100.0	848	15	069990	Q69990 human immun
277	35	100.0	748	15	08J583	Q8j583 human immun	350	35	100.0	848	15	07ZB21	Q7zb21 human immun
278	35	100.0	748	15	08J581	Q8j581 human immun	351	35	100.0	849	15	074849	Q74849 human immun
279	35	100.0	752	15	070604	Q70604 human immun	352	35	100.0	849	15	09PX85	Q9px85 human immun
280	35	100.0	752	15	070605	Q70605 human immun	353	35	100.0	849	15	077368	Q77368 human immun
281	35	100.0	752	15	070608	Q70608 human immun	354	35	100.0	849	15	09PX00	Q9px00 human immun
282	35	100.0	756	15	099BW9	Q99bw9 human immun	355	35	100.0	849	15	011944	Q11944 human immun
283	35	100.0	756	16	0928P8	Q928p8 listeria in	356	35	100.0	849	15	09IBN3	Q9ibn3 human immun
284	35	100.0	757	15	09Q722	Q9q722 human immun	357	35	100.0	849	15	08Q851	Q8q851 human immun
285	35	100.0	766	15	090VG2	Q90vg2 human immun	358	35	100.0	849	15	09YUY1	Q9yuy1 human immun
286	35	100.0	781	15	070159	Q70159 human immun	359	35	100.0	849	15	07ZJJ1	Q7zjj1 human immun
287	35	100.0	783	15	099BX4	Q99bx4 human immun	360	35	100.0	849	15	07ZC14	Q7zcl4 human immun
288	35	100.0	785	15	099BX2	Q99bx2 human immun	361	35	100.0	849	15	07ZC12	Q7zcl2 human immun
289	35	100.0	788	15	099BY6	Q99by6 human immun	362	35	100.0	849	15	07ZC10	Q7zcl0 human immun
290	35	100.0	789	15	09QKJ4	Q9qkj4 human immun	363	35	100.0	849	15	07SV13	Q7sv13 human immun
291	35	100.0	790	15	099BW8	Q99bw8 human immun	364	35	100.0	849	15	078KG4	Q78kg4 human immun
292	35	100.0	790	15	099BY4	Q99by4 human immun	365	35	100.0	850	15	041591	Q41591 human immun
293	35	100.0	791	15	099BX1	Q99bx1 human immun	366	35	100.0	850	15	08UL57	Q8ul57 human immun
294	35	100.0	793	15	099BX8	Q99bx8 human immun	367	35	100.0	850	15	070003	Q70003 human immun
295	35	100.0	795	15	099BX6	Q99bx6 human immun	368	35	100.0	850	15	011946	Q11946 human immun
296	35	100.0	797	15	091W14	Q91w14 human immun	369	35	100.0	850	15	079795	Q79795 human immun
297	35	100.0	797	15	099BY2	Q99by2 human immun	370	35	100.0	850	15	08Q2F2	Q8q2f2 human immun
298	35	100.0	799	15	099BX5	Q99bx5 human immun	371	35	100.0	850	15	09WLG7	Q9wlg7 human immun
299	35	100.0	800	15	099BY1	Q99by1 human immun	372	35	100.0	850	15	08UL56	Q8ul56 human immun
300	35	100.0	801	15	099BY7	Q99by7 human immun	373	35	100.0	850	15	08UL58	Q8ul58 human immun
301	35	100.0	801	15	099BY0	Q99by0 human immun	374	35	100.0	850	15	07SV14	Q7sv14 human immun
302	35	100.0	801	15	099BX0	Q99bx0 human immun	375	35	100.0	851	15	0994B6	Q994b6 human immun
303	35	100.0	801	15	099BX7	Q99bx7 human immun	376	35	100.0	851	15	056110	Q56110 human immun
304	35	100.0	805	15	099BY5	Q99by5 human immun	377	35	100.0	851	15	08Q852	Q8q852 human immun
305	35	100.0	807	15	08Q2X2	Q8q2x2 human immun	378	35	100.0	851	15	073361	Q73361 human immun
306	35	100.0	829	15	076122	Q76122 human immun	379	35	100.0	851	15	078243	Q78243 human immun
307	35	100.0	829	15	07SUQ4	Q7suq4 human immun	380	35	100.0	851	15	09E1R6	Q9e1r6 human immun
308	35	100.0	829	15	07SUQ3	Q7suq3 human immun	381	35	100.0	851	15	056562	Q56562 human immun

382	35	100.0	851	15	Q73304	human immun
383	35	100.0	851	15	Q73365	human immun
384	35	100.0	851	15	Q7SV38	human immun
385	35	100.0	852	15	Q41580	human immun
386	35	100.0	852	15	Q69992	human immun
387	35	100.0	852	15	Q8UL55	human immun
388	35	100.0	852	15	Q8UL54	human immun
389	35	100.0	852	15	Q9DL88	human immun
390	35	100.0	852	15	Q92761	human immun
391	35	100.0	852	15	Q8UL59	human immun
392	35	100.0	852	15	Q73303	human immun
393	35	100.0	852	15	Q41885	human immun
394	35	100.0	852	15	Q41546	human immun
395	35	100.0	852	15	Q89797	human immun
396	35	100.0	852	15	Q41883	human immun
397	35	100.0	852	15	Q76120	human immun
398	35	100.0	852	15	Q41593	human immun
399	35	100.0	852	15	Q56567	human immun
400	35	100.0	852	15	Q70006	human immun
401	35	100.0	852	15	Q7SVL5	human immun
402	35	100.0	853	15	Q73372	human immun
403	35	100.0	853	15	Q80161	human immun
404	35	100.0	853	15	Q70202	human immun
405	35	100.0	853	15	Q9E1S9	human immun
406	35	100.0	853	15	Q56108	human immun
407	35	100.0	853	15	Q9DL91	human immun
408	35	100.0	853	15	Q9DL93	human immun
409	35	100.0	853	15	Q9DL89	human immun
410	35	100.0	853	15	Q8UPN0	human immun
411	35	100.0	853	15	Q55774	human immun
412	35	100.0	853	15	Q8JCL7	human immun
413	35	100.0	853	15	Q9YUY6	human immun
414	35	100.0	853	15	Q56563	human immun
415	35	100.0	853	15	Q8AF21	human immun
416	35	100.0	853	15	Q8AE50	human immun
417	35	100.0	853	15	Q7ZJF5	human immun
418	35	100.0	853	15	Q7SVL6	human immun
419	35	100.0	853	15	Q7SUR3	human immun
420	35	100.0	853	15	Q7SUR2	human immun
421	35	100.0	853	15	Q7S1K0	human immun
422	35	100.0	854	15	Q56566	human immun
423	35	100.0	854	15	Q85582	human immun
424	35	100.0	854	15	Q56319	simian-huma
425	35	100.0	854	15	Q72502	human immun
426	35	100.0	854	15	Q91JZ7	human immun
427	35	100.0	854	15	Q9E1S0	human immun
428	35	100.0	854	15	Q90178	human immun
429	35	100.0	854	15	Q70020	human immun
430	35	100.0	854	15	Q9DKG6	human immun
431	35	100.0	854	15	Q40222	human immun
432	35	100.0	854	15	Q92762	human immun
433	35	100.0	854	15	Q56112	human immun
434	35	100.0	854	15	Q69998	human immun
435	35	100.0	854	15	Q8UPM1	human immun
436	35	100.0	854	15	Q9E1S8	human immun
437	35	100.0	854	15	Q78225	human immun
438	35	100.0	854	15	Q78705	human immun
439	35	100.0	854	15	Q91JZ9	human immun
440	35	100.0	854	15	Q7ZBZ9	human immun
441	35	100.0	854	15	Q7SVL3	human immun
442	35	100.0	854	15	Q7SUC9	human immun
443	35	100.0	854	15	Q7SUC8	human immun
444	35	100.0	854	15	Q7SUC7	human immun
445	35	100.0	854	15	Q7SUC6	human immun
446	35	100.0	854	15	Q7SUC5	human immun
447	35	100.0	854	15	Q7SQM8	human immun
448	35	100.0	854	15	Q7S1I2	human immun
449	35	100.0	855	15	Q8UL61	human immun
450	35	100.0	855	15	Q8Q367	human immun
451	35	100.0	855	15	Q9YUY3	human immun
452	35	100.0	855	15	Q8UL64	human immun
453	35	100.0	855	15	Q8UL60	human immun
454	35	100.0	855	15	Q8UL62	human immun
455	35	100.0	855	15	Q9E1R7	human immun
456	35	100.0	855	15	Q74841	human immun
457	35	100.0	855	15	Q9DL90	human immun
458	35	100.0	855	15	Q70016	human immun
459	35	100.0	855	15	Q9DL76	human immun
460	35	100.0	855	15	Q91K00	human immun
461	35	100.0	855	15	Q902H5	human immun
462	35	100.0	855	15	Q9DL92	human immun
463	35	100.0	855	15	Q03805	human immun
464	35	100.0	855	15	Q8AQV7	human immun
465	35	100.0	855	15	Q7SVL0	human immun
466	35	100.0	855	15	Q7SUS7	human immun
467	35	100.0	855	15	Q7SUS6	human immun
468	35	100.0	855	15	Q7SUS5	human immun
469	35	100.0	855	15	Q7SUS4	human immun
470	35	100.0	855	15	Q7SUS3	human immun
471	35	100.0	855	15	Q7SUS2	human immun
472	35	100.0	855	15	Q7SUS1	human immun
473	35	100.0	855	15	Q7SUS0	human immun
474	35	100.0	855	15	Q7SUR9	human immun
475	35	100.0	855	15	Q7SUR8	human immun
476	35	100.0	855	15	Q7SUR7	human immun
477	35	100.0	855	15	Q7SUR6	human immun
478	35	100.0	855	15	Q7SUR5	human immun
479	35	100.0	855	15	Q7SUR4	human immun
480	35	100.0	855	15	Q7SUR1	human immun
481	35	100.0	855	15	Q7SUR0	human immun
482	35	100.0	856	15	Q9SC06	human immun
483	35	100.0	856	15	Q9E1S5	human immun
484	35	100.0	856	15	P90115	human immun
485	35	100.0	856	15	Q41539	human immun
486	35	100.0	856	15	Q73296	human immun
487	35	100.0	856	15	Q9YUY5	human immun
488	35	100.0	856	15	Q9YUY4	human immun
489	35	100.0	856	15	Q9FXZ0	human immun
490	35	100.0	856	15	Q74090	human immun
491	35	100.0	856	15	Q9DSL8	human immun
492	35	100.0	856	15	Q9OSM7	human immun
493	35	100.0	856	15	Q71014	human immun
494	35	100.0	856	15	Q9E1R8	human immun
495	35	100.0	856	15	Q92877	simian-huma
496	35	100.0	856	15	Q70200	human immun
497	35	100.0	856	15	Q73295	human immun
498	35	100.0	856	15	Q74599	human immun
499	35	100.0	856	15	Q41772	human immun
500	35	100.0	856	15	Q72993	human immun

ALIGNMENTS

RESULT 1

Q69904	PRELIMINARY;	PRT;	34 AA.
ID Q69904			
AC Q69904;			
DT 01-NOV-1996 (TrEMBLrel. 01, Created)			
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE Gp41 (Fragment).			
GN ENV.			
OS Human immunodeficiency virus 1.			
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX NCBI_TaxID=11676;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=94211861; PubMed=7512731;			
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,			
RA Keller P.M., Shaw A.R., Emini E.A.;			
RT "Neutralization of divergent human immunodeficiency virus type 1			
RT variants and primary isolates by IAM-41-2P5, an anti-gp41 human			
RT monoclonal antibody.";			
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).			
DR EMBL; U06734; AAA19147.1; -.			

```

DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4184 MW; BB1CAA65F131AD5A CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 2
Q69905 PRELIMINARY; PRT; 34 AA.
AC Q69905;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4196 MW; 7B724A8EA164BD9C CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 3
Q69893 PRELIMINARY; PRT; 34 AA.
AC Q69893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4196 MW; 7B724A8EA164BD9C CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 4
Q69903 PRELIMINARY; PRT; 34 AA.
AC Q69903;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4226 MW; E609273F6164BD80 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 5
Q69894 PRELIMINARY; PRT; 34 AA.
AC Q69894;

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4196 MW; 0C7CAA60A164B89C CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 4
Q69903 PRELIMINARY; PRT; 34 AA.
AC Q69903;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4226 MW; E609273F6164BD80 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 5
Q69894 PRELIMINARY; PRT; 34 AA.
AC Q69894;

```



```

KW Transmembrane.
FT NON_TER 1
  42
SQ SEQUENCE 42 AA; 5248 MW; 613E1B2DBB31A722 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.9; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 1 ELDKWA 6
  |||||
Db 31 ELDKWA 36

RESULT 9
ID Q69896 PRELIMINARY; PRT; 49 AA.
AC Q69896;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
  Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
  variants and primary isolates by IAM-41-2F5, an anti-gp41 human
  monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06726; AAA19139.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
  49
SQ SEQUENCE 49 AA; 6167 MW; 0277C4815B8D26FE CRC64;

Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 1 ELDKWA 6
  |||||
Db 38 ELDKWA 43

RESULT 10
ID Q69906 PRELIMINARY; PRT; 49 AA.
AC Q69906;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
  Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
  variants and primary isolates by IAM-41-2F5, an anti-gp41 human
  monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06726; AAA19139.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
  49
SQ SEQUENCE 49 AA; 6167 MW; 0277C4815B8D26FE CRC64;

Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 1 ELDKWA 6
  |||||
Db 38 ELDKWA 43

RESULT 11
ID Q69907 PRELIMINARY; PRT; 49 AA.
AC Q69907;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
  Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
  variants and primary isolates by IAM-41-2F5, an anti-gp41 human
  monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06737; AAA19150.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
  49
SQ SEQUENCE 49 AA; 6214 MW; 29C4E5A8CBDC7CDD8 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 1 ELDKWA 6
  |||||
Db 38 ELDKWA 43

RESULT 12
ID Q69895 PRELIMINARY; PRT; 49 AA.
AC Q69895;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.

```

```

RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
  monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06736; AAA19149.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
  49
SQ SEQUENCE 49 AA; 6214 MW; 29C4E5A8CBDC7CDD8 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 1 ELDKWA 6
  |||||
Db 38 ELDKWA 43

RESULT 11
ID Q69907 PRELIMINARY; PRT; 49 AA.
AC Q69907;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
  Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
  variants and primary isolates by IAM-41-2F5, an anti-gp41 human
  monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06737; AAA19150.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
  49
SQ SEQUENCE 49 AA; 6214 MW; 29C4E5A8CBDC7CDD8 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 1 ELDKWA 6
  |||||
Db 38 ELDKWA 43

RESULT 12
ID Q69895 PRELIMINARY; PRT; 49 AA.
AC Q69895;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.

```

```
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06725; AAA19138.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 49
FT NON_TER 49
SQ SEQUENCE 49 AA; 6168 MW; 8077C4815B83281E CRC64;

Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 38 ELDKWA 43

RESULT 13
ID Q69909 PRELIMINARY; PRT; 49 AA.
AC Q69909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06739; AAA19152.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 49
FT NON_TER 49
SQ SEQUENCE 49 AA; 6196 MW; E9B618825B832D1E CRC64;

Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 38 ELDKWA 43

RESULT 14
ID Q69898 PRELIMINARY; PRT; 50 AA.
AC Q69898;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06728; AAA19141.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 50
FT NON_TER 50
SQ SEQUENCE 50 AA; 6358 MW; EABA093A1C6C79E1 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 39 ELDKWA 44

RESULT 15
ID Q69913 PRELIMINARY; PRT; 57 AA.
AC Q69913;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06743; AAA19156.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 57
FT NON_TER 57
SQ SEQUENCE 57 AA; 7195 MW; D9AC849ED459FD04 CRC64;
```



```

Query Match      100.0%; Score 35; DB 15; Length 57;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      46 ELDRKA 51
      |||||

RESULT 16
Q69912      PRELIMINARY;      PRT;      57 AA.
AC Q69912;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06742; AAA19154.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 57
SQ SEQUENCE 57 AA; 7123 MW; D9AC849C76D3D704 CRC64;

Query Match      100.0%; Score 35; DB 15; Length 57;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      46 ELDRKA 51
      |||||

RESULT 17
Q69911      PRELIMINARY;      PRT;      57 AA.
AC Q69911;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06741; AAA19154.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.

```

```

DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 57
SQ SEQUENCE 57 AA; 7267 MW; C2BC6A9034525CAE CRC64;

Query Match      100.0%; Score 35; DB 15; Length 57;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      46 ELDRKA 51
      |||||

RESULT 18
Q9QQN5      PRELIMINARY;      PRT;      117 AA.
AC Q9QQN5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=96USHS97;
RA Ellenberger D., Sullivan P.S., Dorn J., Schable C., Spira T.J.,
RA Folks T.M., Lal R.B.;
RT "Viral and Immunologic Examination of HIV-1-infected Persistently
RT Seronegative (HIPS) Persons."
RL J. Infect. Dis. 0:0-0(1999).
DR EMBL; AF157468; AAD45888.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14011 MW; 9A71687C21470B60 CRC64;

Query Match      100.0%; Score 35; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      102 ELDRKA 107
      |||||

RESULT 19
Q9YRS9      PRELIMINARY;      PRT;      117 AA.
AC Q9YRS9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=96USSN94;

```

```
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096337; AAD04412.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13953 MW; FIA8174D1A50B77B CRC64;

Query Match 100.0%; Score 35; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 20
Q9YYW7 Q9YYW7 PRELIMINARY; PRT; 117 AA.
AC Q9YYW7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=326.661;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006939; AAD01383.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13911 MW; CD3E75531269F9C7 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 106 ELDKWA 111

RESULT 21
Q9YRS2 Q9YRS2 PRELIMINARY; PRT; 117 AA.
AC Q9YRS2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
```

```
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USTG17;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096344; AAD04419.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 14004 MW; 11CA37F5C8C6278F CRC64;

Query Match 100.0%; Score 35; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 22
Q9YYW1 Q9YYW1 PRELIMINARY; PRT; 117 AA.
AC Q9YYW1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=503.083;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006951; AAD01395.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 14043 MW; 76573E01C889F22C CRC64;

Query Match 100.0%; Score 35; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 106 ELDKWA 111
```

```

RESULT 23
Q9ESR1
ID AC Q9ESR1 PRELIMINARY; PRT; 118 AA.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM188;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon.";
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM188;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemnji G.A., Eno L.T.,
RA Ngngasong J.N., Gao F., Rayfield M., Folks T.M., Pieniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252110; AAG14319.1; -.
DR GO; GO:0016031; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane. 1
KW Transmembrane. 1
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 14377 MW; D972C44345FA07D3 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 98 ELDKWA 103

RESULT 24
Q9ESS3
ID AC Q9ESS3 PRELIMINARY; PRT; 118 AA.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM11;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon.";
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM11;

```

```

RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemnji G.A., Eno L.T.,
RA Ngngasong J.N., Gao F., Rayfield M., Folks T.M., Pieniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252098; AAG14307.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane. 1
KW Transmembrane. 1
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 14275 MW; 1878D17C292899C0 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 98 ELDKWA 103

```

```

RESULT 25
Q9ESS2
ID AC Q9ESS2 PRELIMINARY; PRT; 118 AA.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM110;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon.";
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM110;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemnji G.A., Eno L.T.,
RA Ngngasong J.N., Gao F., Rayfield M., Folks T.M., Pieniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252099; AAG14308.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane. 1
KW Transmembrane. 1
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 14288 MW; 051B1921BA69276A CRC64;

Query Match 100.0%; Score 35; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 98 ELDKWA 103

```

RESULT 26

```
Q9YZ02
ID Q9YZ02 PRELIMINARY; PRT; 118 AA.
AC Q9YZ02;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RC STRAIN=151.940;
RA Brennan C.A., Lund J.K., Golden A., Yanaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006870; AA001314.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 14076 MW; 6FB855B3B1FC23F CRC64;

Query Match 100.0%; Score 35; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
DB 107 ELDKWA 112
|||||

RESULT 27
Q9EA94
ID Q9EA94 PRELIMINARY; PRT; 122 AA.
AC Q9EA94;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=BX513;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190958; AAG02320.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14674 MW; AFDA96E7701E7E5B CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
```

```
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
DB 102 ELDKWA 107
|||||

RESULT 28
Q9YXN9
ID Q9YXN9 PRELIMINARY; PRT; 122 AA.
AC Q9YXN9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=RU96BRP089;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034064; AAC79316.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14636 MW; C42C7A900C8C1DB8 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
DB 102 ELDKWA 107
|||||

RESULT 29
Q9EA85
ID Q9EA85 PRELIMINARY; PRT; 122 AA.
AC Q9EA85;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=BX84;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190967; AAG02329.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
```

```
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14692 MW; F777D665CE19C4E0 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107
|||||

RESULT 30
Q9EA81 PRELIMINARY; PRT; 122 AA.
AC Q9EA81;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX923;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190971; AAG02333.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14753 MW; C3FE4DB1F8B5BCBD CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107
|||||

RESULT 31
Q9YXQ0 PRELIMINARY; PRT; 122 AA.
AC Q9YXQ0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RX96BRP043;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034053; AAC79305.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14733 MW; B008FE9FF1F36D0C CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107
|||||

RESULT 32
Q9QIW4 PRELIMINARY; PRT; 122 AA.
AC Q9QIW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ07;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165540; AAF08485.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14742 MW; B42975291BA5F682 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107
|||||

RESULT 33
Q9EAA4 PRELIMINARY; PRT; 122 AA.
AC Q9EAA4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
```

```

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX157;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidie P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190948; C:integral to membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1 122
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14805 MW; D5C7A228B3538108B CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 34
Q9QIWO PRELIMINARY; PRT; 122 AA.
AC Q9QIWO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ11;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165544; AAF08489.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1 122
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14716 MW; CB39CB85DADE28FE CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 35
Q9IUNI PRELIMINARY; PRT; 122 AA.
AC Q9IUNI;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR52;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220701; AAF76820.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1 122
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14917 MW; 69477A001A80725D CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 36
Q9WQZO PRELIMINARY; PRT; 122 AA.
AC Q9WQZO;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TH38;
RA Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113592; AAD42760.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1 122
FT NON_TER 122 122
```

```
SQ SEQUENCE 122 AA; 14860 MW; 9F379DA806F98CED CRC64;
Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 102 ELDKWA 107

RESULT 37
Q9YXR6 PRELIMINARY; PRT; 122 AA.
ID Q9YXR6
AC Q9YXR6
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP004;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A., D.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.,
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034037; AAC79289.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14702 MW; 873C9A28AE14BA78 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 102 ELDKWA 107

RESULT 38
Q9QIU3 PRELIMINARY; PRT; 122 AA.
ID Q9QIU3
AC Q9QIU3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ28;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165561; AAF08506.1; -.
```

```
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
KW NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14817 MW; 8D6099E5D3993205 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 102 ELDKWA 107

RESULT 39
Q9EAA5 PRELIMINARY; PRT; 122 AA.
ID Q9EAA5
AC Q9EAA5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX126;
RX MEDLINE=20134570; Pubmed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190947; AAG02309.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
KW NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14859 MW; E6D2DAD15E71607A CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 102 ELDKWA 107

RESULT 40
Q9IJM8 PRELIMINARY; PRT; 122 AA.
ID Q9IJM8
AC Q9IJM8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
```

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=AR58;
RX  MEDLINE=20346416; PubMed=10890362;
RA  Masciotra S., Livellara B., Dellosa W., Clara L., Tanuri A., Ramos A.,
RA  Baggs J., Lal R., Pieniazek D.,
RT  "Evidence for a high frequency of HIV-1 subtype F infections among
RT  heterosexual population in Buenos Aires, Argentina.";
RL  AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR  EMBL; AF220704; AAF76823.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0019031; C:viral envelope; IEA.
DR  GO; GO:0005198; F:structural molecule activity; IEA.
DR  InterPro; IPR000328; Env_GP41.
DR  Pfam; PF00517; GP41; 1.
KW  Transmembrane.
FT  NON_TER 1
FT  NON_TER 122
SQ  SEQUENCE 122 AA; 14735 MW; 040891ADC152BEE4 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 41
Q9EAA2 PRELIMINARY; PRT; 122 AA.
AC Q9EAA2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20134570; PubMed=10669328;
RA Wetle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190950; AAG02312.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14751 MW; 302E5D7E45ED007D CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 42
Q90PX7 PRELIMINARY; PRT; 122 AA.
AC Q90PX7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=211270244; PubMed=11376043;
RA Agwale S.M., Robbins K.E., Odama L., Saekhou A., Zeh C., Eubio A.,
RA Njoku O.M., Sani-Gwarzo N., Gboun M.F., Gao F., Reitz M., Hone D.,
RA Folks T.M., Pieniazek D., Wambebe C., Kalish M.L.;
RT "Development of an env gp41-based Heteroduplex Mobility Assay for
RT Rapid Human Immunodeficiency Virus Type 1 Subtyping.";
RL J. Clin. Microbiol. 39:2110-2114(2001).
DR EMBL; AF343909; AAK66176.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14701 MW; 6A9C8669908E6F1E CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 43
Q9WQZ1 PRELIMINARY; PRT; 122 AA.
AC Q9WQZ1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TH27;
RA Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113591; AAD42759.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14847 MW; 4E202AEC6B404A06 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


QY 1 ELDKWA 6
KW Transmembrane. 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14821 MW; AB7E4230D257A34E CRC64;
Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 44
Q9EAG9 PRELIMINARY; PRT; 122 AA.
AC Q9EAG9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BK380;
RC MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.;
RL J. Infect. Dis. 181:470-475 (2000).
DR EMBL; AF190953; AAC02315.1; -;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
KW Transmembrane. 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14671 MW; C925320AF179C213 CRC64;
Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
KW Transmembrane. 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14671 MW; C925320AF179C213 CRC64;
Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 45
Q9YXR8 PRELIMINARY; PRT; 122 AA.
AC Q9YXR8;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RU96BRP001;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil";
RT Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034035; AAC79287.1; -;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.

DR Pfam; PF00517; GP41; 1.
KW Transmembrane. 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14821 MW; AB7E4230D257A34E CRC64;
Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
KW Transmembrane. 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14821 MW; AB7E4230D257A34E CRC64;
Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 46
Q9LJN5 PRELIMINARY; PRT; 122 AA.
AC Q9LJN5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AR36;
RC MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR EMBL; AF220697; AAF76816.1; -;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
KW Transmembrane. 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14779 MW; C9B2C8944C48C614 CRC64;
Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
KW Transmembrane. 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14779 MW; C9B2C8944C48C614 CRC64;
Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 47
Q9WQY8 PRELIMINARY; PRT; 122 AA.
AC Q9WQY8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TH89;
RA Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O

```
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113594; AAD42762.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14816 MW; 3F9D3FAD52DC0503 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
DB 102 ELDKWA 107
|||||

RESULT 48
Q91JQ0 PRELIMINARY; PRT; 122 AA.
AC Q91JQ0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR8;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S.; Livellara B.; Bellosio W.; Clara L.; Tanuri A.; Ramos A.;
RA Baggs J.; Lal R.; Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220682; AAF74234.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14549 MW; 7C9AE589350B76B5 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
DB 102 ELDKWA 107
|||||

RESULT 49
Q9YXP7 PRELIMINARY; PRT; 122 AA.
AC Q9YXP7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
```

```
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP065;
RA Tanuri A.; Swanson P.A.; Devare S.G.; Berro O.J.; Savedra A.;
RA Costa L.J.; Telles J.G.; Brindeiro R.; Schable C.; Pieniazek D.;
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034056; AAC79308.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14791 MW; A96F27C55B01E4CD CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
DB 102 ELDKWA 107
|||||

RESULT 50
Q9WQZ7 PRELIMINARY; PRT; 122 AA.
AC Q9WQZ7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CN37;
RA Pieniazek D.; Yang C.; Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113585; AAD42753.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14807 MW; 7744F5AF97830718 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
DB 102 ELDKWA 107
|||||

Search completed: March 16, 2004, 09:17:46
Job time : 49 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2004, 09:15:21 ; Search time 22 Seconds
(without alignments)
14.080 Million cell up

Title: US-10-024-329-2

Perfect score: 35

Sequence: 1 BLDKWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum D8 seq length: 0

Maximum DB seq length: 2000000000
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0% Maximum Match 100%

Maximum Match 100%
Listing first 500 summaries

Database : Issued Patents AA:*

1: /cqn2 6/ptodata/2/iaa/5A COMB.pcp:*

2: /cgn2 6/ptodata/2/iaa/5B_COMB.pcp: *

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pcp:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pcp.*

5: /cgn2_6/ptodata/2/iaa/pCTUS_COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	35	100.0	6	1	US-08-257-528B-69	Sequence 69, Appl
2	35	100.0	6	1	US-08-361-479-1	Sequence 1, Appli
3	35	100.0	6	1	US-08-473-576-1	Sequence 69, Appl
4	35	100.0	6	1	US-08-460-602A-69	Sequence 47, Appl
5	35	100.0	6	1	US-08-323-192D-47	Sequence 69, Appl
6	35	100.0	6	1	US-08-463-966A-69	Sequence 69, Appl
7	35	100.0	6	1	US-08-465-217A-69	Sequence 69, Appl
8	35	100.0	6	2	US-08-464-329A-69	Sequence 1, Appli
9	35	100.0	6	2	US-08-021-879-1	Sequence 46, Appl
10	35	100.0	6	2	US-08-470-887A-46	Sequence 46, Appl
11	35	100.0	6	2	US-08-252-508B-46	Sequence 23, Appl
12	35	100.0	6	2	US-08-975-699-23	Sequence 23, Appl
13	35	100.0	6	2	US-08-417-210A-147	Sequence 147, App
14	35	100.0	6	2	US-08-843-718-1	Sequence 1, Appli
15	35	100.0	6	2	US-08-462-507A-69	Sequence 69, Appl
16	35	100.0	6	2	US-08-972-089-23	Sequence 23, Appl
17	35	100.0	6	2	US-08-467-881A-69	Sequence 69, Appl
18	35	100.0	6	3	US-09-106-377-46	Sequence 46, Appl
19	35	100.0	6	3	US-09-124-900-11	Sequence 11, Appl
20	35	100.0	6	4	US-09-340-798A-53	Sequence 53, Appl
21	35	100.0	6	4	US-09-136-159A-147	Sequence 147, App
22	35	100.0	6	4	US-09-525-874-1	Sequence 1, Appli
23	35	100.0	6	4	US-09-873-459A-4	Sequence 4, Appli
24	35	100.0	7	1	US-08-257-528B-98	Sequence 98, Appl
25	35	100.0	7	1	US-08-460-602A-98	Sequence 98, Appl
26	35	100.0	7	1	US-08-463-966A-98	Sequence 98, Appl
27	35	100.0	7	1	US-08-465-217A-98	Sequence 98, Appl

101	35	100.0	13	4	US-09-315-304B-267	Sequence 267, App	174	35	100.0	15	3	US-08-486-099-167	Sequence 167, App
102	35	100.0	13	4	US-09-315-304B-268	Sequence 268, App	175	35	100.0	15	3	US-08-486-099-168	Sequence 168, App
103	35	100.0	13	4	US-09-315-304B-269	Sequence 269, App	176	35	100.0	15	3	US-08-484-223B-166	Sequence 166, App
104	35	100.0	13	4	US-09-315-304B-270	Sequence 270, App	177	35	100.0	15	3	US-08-484-223B-167	Sequence 167, App
105	35	100.0	13	4	US-09-315-304B-530	Sequence 530, App	178	35	100.0	15	3	US-08-484-223B-168	Sequence 168, App
106	35	100.0	13	4	US-09-315-304B-531	Sequence 531, App	179	35	100.0	15	3	US-08-919-597-166	Sequence 166, App
107	35	100.0	13	4	US-08-973-952-22	Sequence 22, App1	180	35	100.0	15	3	US-08-919-597-167	Sequence 167, App
108	35	100.0	13	4	US-08-973-952-23	Sequence 23, App1	181	35	100.0	15	3	US-08-919-597-168	Sequence 168, App
109	35	100.0	13	4	US-08-973-952-24	Sequence 24, App1	182	35	100.0	15	3	US-08-475-668A-166	Sequence 166, App
110	35	100.0	13	4	US-08-973-952-25	Sequence 25, App1	183	35	100.0	15	3	US-08-475-668A-167	Sequence 167, App
111	35	100.0	13	4	US-08-973-952-26	Sequence 26, App1	184	35	100.0	15	3	US-08-475-668A-168	Sequence 168, App
112	35	100.0	13	4	US-08-470-896-169	Sequence 169, App	185	35	100.0	15	3	US-08-485-551A-166	Sequence 166, App
113	35	100.0	13	4	US-08-470-896-170	Sequence 170, App	186	35	100.0	15	3	US-08-485-551A-167	Sequence 167, App
114	35	100.0	13	4	US-08-470-896-171	Sequence 171, App	187	35	100.0	15	3	US-08-485-551A-168	Sequence 168, App
115	35	100.0	13	4	US-08-470-896-172	Sequence 172, App	188	35	100.0	15	3	US-08-471-913A-166	Sequence 166, App
116	35	100.0	13	4	US-08-470-896-173	Sequence 173, App	189	35	100.0	15	3	US-08-471-913A-167	Sequence 167, App
117	35	100.0	13	4	US-08-485-546A-169	Sequence 169, App	190	35	100.0	15	3	US-08-471-913A-168	Sequence 168, App
118	35	100.0	13	4	US-08-485-546A-170	Sequence 170, App	191	35	100.0	15	3	US-08-554-616-54	Sequence 54, App1
119	35	100.0	13	4	US-08-485-546A-171	Sequence 171, App	192	35	100.0	15	3	US-08-485-264A-166	Sequence 166, App
120	35	100.0	13	4	US-08-485-546A-172	Sequence 172, App	193	35	100.0	15	3	US-08-485-264A-167	Sequence 167, App
121	35	100.0	13	4	US-08-485-546A-173	Sequence 173, App	194	35	100.0	15	3	US-08-485-264A-168	Sequence 168, App
122	35	100.0	13	4	US-08-834-784-218	Sequence 218, App	195	35	100.0	15	3	US-09-082-279B-216	Sequence 216, App
123	35	100.0	13	4	US-08-834-784-267	Sequence 267, App	196	35	100.0	15	3	US-09-082-279B-372	Sequence 372, App
124	35	100.0	13	4	US-08-834-784-268	Sequence 268, App	197	35	100.0	15	3	US-09-082-279B-373	Sequence 373, App
125	35	100.0	13	4	US-08-834-784-269	Sequence 269, App	198	35	100.0	15	3	US-09-082-279B-513	Sequence 513, App
126	35	100.0	13	4	US-08-834-784-270	Sequence 270, App	199	35	100.0	15	3	US-09-082-279B-514	Sequence 514, App
127	35	100.0	13	4	US-08-834-784-530	Sequence 530, App	200	35	100.0	15	3	US-09-082-279B-515	Sequence 515, App
128	35	100.0	13	4	US-08-834-784-531	Sequence 531, App	201	35	100.0	15	3	US-09-082-279B-792	Sequence 792, App
129	35	100.0	13	4	US-09-515-965A-218	Sequence 218, App	202	35	100.0	15	3	US-08-474-349A-166	Sequence 166, App
130	35	100.0	13	4	US-09-515-965A-267	Sequence 267, App	203	35	100.0	15	4	US-08-474-349A-167	Sequence 167, App
131	35	100.0	13	4	US-09-515-965A-268	Sequence 268, App	204	35	100.0	15	4	US-08-474-349A-167	Sequence 168, App
132	35	100.0	13	4	US-09-515-965A-269	Sequence 269, App	205	35	100.0	15	4	US-08-474-349A-426	Sequence 426, App
133	35	100.0	13	4	US-09-515-965A-270	Sequence 270, App	206	35	100.0	15	4	US-08-474-349A-430	Sequence 430, App
134	35	100.0	13	4	US-09-515-965A-530	Sequence 530, App	207	35	100.0	15	4	US-08-474-349A-431	Sequence 431, App
135	35	100.0	13	4	US-09-515-965A-531	Sequence 531, App	208	35	100.0	15	4	US-08-474-349A-432	Sequence 432, App
136	35	100.0	13	4	US-09-350-641C-218	Sequence 218, App	209	35	100.0	15	4	US-09-315-304B-216	Sequence 216, App
137	35	100.0	13	4	US-09-350-641C-267	Sequence 267, App	210	35	100.0	15	4	US-09-315-304B-372	Sequence 372, App
138	35	100.0	13	4	US-09-350-641C-268	Sequence 268, App	211	35	100.0	15	4	US-09-315-304B-373	Sequence 373, App
139	35	100.0	13	4	US-09-350-641C-269	Sequence 269, App	212	35	100.0	15	4	US-09-315-304B-374	Sequence 374, App
140	35	100.0	13	4	US-09-350-641C-270	Sequence 270, App	213	35	100.0	15	4	US-09-315-304B-513	Sequence 513, App
141	35	100.0	13	4	US-09-350-641C-530	Sequence 530, App	214	35	100.0	15	4	US-09-315-304B-515	Sequence 514, App
142	35	100.0	13	4	US-09-350-641C-531	Sequence 531, App	215	35	100.0	15	4	US-09-315-304B-515	Sequence 515, App
143	35	100.0	14	1	US-08-073-028-53	Sequence 53, App1	216	35	100.0	15	4	US-08-973-952-19	Sequence 19, App1
144	35	100.0	14	3	US-08-554-616-53	Sequence 53, App1	217	35	100.0	15	4	US-08-973-952-20	Sequence 20, App1
145	35	100.0	14	3	US-09-082-279B-217	Sequence 217, App	218	35	100.0	15	4	US-08-973-952-21	Sequence 21, App1
146	35	100.0	14	3	US-09-082-279B-219	Sequence 219, App	219	35	100.0	15	4	US-08-470-896-166	Sequence 166, App
147	35	100.0	14	3	US-09-082-279B-229	Sequence 229, App	220	35	100.0	15	4	US-08-470-896-167	Sequence 167, App
148	35	100.0	14	4	US-08-474-349A-427	Sequence 427, App	221	35	100.0	15	4	US-08-470-896-168	Sequence 168, App
149	35	100.0	14	4	US-09-315-304B-217	Sequence 217, App	222	35	100.0	15	4	US-08-485-546A-166	Sequence 166, App
150	35	100.0	14	4	US-09-315-304B-229	Sequence 229, App	223	35	100.0	15	4	US-08-485-546A-167	Sequence 167, App
151	35	100.0	14	4	US-09-834-784-217	Sequence 217, App	224	35	100.0	15	4	US-08-485-546A-168	Sequence 168, App
152	35	100.0	14	4	US-09-834-784-229	Sequence 229, App	225	35	100.0	15	4	US-08-485-546A-168	Sequence 216, App
153	35	100.0	14	4	US-09-515-965A-217	Sequence 217, App	226	35	100.0	15	4	US-09-834-784-216	Sequence 372, App
154	35	100.0	14	4	US-09-515-965A-229	Sequence 229, App	227	35	100.0	15	4	US-09-834-784-372	Sequence 373, App
155	35	100.0	14	4	US-09-515-965A-1666	Sequence 1666, App	228	35	100.0	15	4	US-09-834-784-373	Sequence 374, App
156	35	100.0	14	4	US-09-350-641C-217	Sequence 217, App	229	35	100.0	15	4	US-09-834-784-513	Sequence 513, App
157	35	100.0	14	4	US-09-350-641C-229	Sequence 229, App	230	35	100.0	15	4	US-09-834-784-514	Sequence 514, App
158	35	100.0	15	1	US-08-073-028-54	Sequence 54, App1	231	35	100.0	15	4	US-09-834-784-515	Sequence 515, App
159	35	100.0	15	1	US-08-257-528B-59	Sequence 59, App1	232	35	100.0	15	4	US-09-834-784-792	Sequence 792, App
160	35	100.0	15	1	US-08-257-528B-93	Sequence 93, App1	233	35	100.0	15	4	US-09-515-965A-216	Sequence 216, App
161	35	100.0	15	1	US-08-460-602A-59	Sequence 59, App1	234	35	100.0	15	4	US-09-515-965A-372	Sequence 372, App
162	35	100.0	15	1	US-08-460-602A-93	Sequence 93, App1	235	35	100.0	15	4	US-09-515-965A-373	Sequence 373, App
163	35	100.0	15	1	US-08-463-966A-59	Sequence 59, App1	236	35	100.0	15	4	US-09-515-965A-374	Sequence 374, App
164	35	100.0	15	1	US-08-463-966A-93	Sequence 93, App1	237	35	100.0	15	4	US-09-515-965A-513	Sequence 513, App
165	35	100.0	15	1	US-08-465-217A-59	Sequence 93, App1	238	35	100.0	15	4	US-09-515-965A-514	Sequence 514, App
166	35	100.0	15	1	US-08-465-217A-93	Sequence 93, App1	239	35	100.0	15	4	US-09-515-965A-792	Sequence 792, App
167	35	100.0	15	2	US-08-464-329A-59	Sequence 59, App1	240	35	100.0	15	4	US-09-515-965A-1667	Sequence 1667, App
168	35	100.0	15	2	US-08-464-329A-93	Sequence 59, App1	241	35	100.0	15	4	US-09-350-641C-216	Sequence 216, App
169	35	100.0	15	2	US-08-462-507A-59	Sequence 59, App1	242	35	100.0	15	4	US-09-350-641C-372	Sequence 372, App
170	35	100.0	15	2	US-08-462-507A-93	Sequence 93, App1	243	35	100.0	15	4	US-09-350-641C-373	Sequence 373, App
171	35	100.0	15	2	US-08-467-881A-59	Sequence 93, App1	244	35	100.0	15	4		
172	35	100.0	15	2	US-08-467-881A-93	Sequence 93, App1	245	35	100.0	15	4		
173	35	100.0	15	3	US-08-486-099-166	Sequence 166, App	246	35	100.0	15	4		

247	35	100.0	15	4	US-09-350-641C-374	Sequence 374, App	320	20	1	US-08-460-602A-55	Sequence 55, Appl
248	35	100.0	15	4	US-09-350-641C-513	Sequence 513, App	321	20	1	US-08-463-966A-55	Sequence 55, Appl
249	35	100.0	15	4	US-09-350-641C-514	Sequence 514, App	322	20	1	US-08-465-217A-55	Sequence 55, Appl
250	35	100.0	15	4	US-09-350-641C-515	Sequence 515, App	323	20	2	US-08-464-329A-55	Sequence 55, Appl
251	35	100.0	15	4	US-09-350-641C-792	Sequence 792, App	324	20	2	US-08-462-507A-55	Sequence 55, Appl
252	35	100.0	16	1	US-08-073-028-55	Sequence 55, Appl	325	20	3	US-08-467-881A-55	Sequence 55, Appl
253	35	100.0	16	3	US-08-554-616-55	Sequence 55, Appl	326	20	3	US-09-071-877-8	Sequence 8, Appl
254	35	100.0	16	3	US-09-082-279B-215	Sequence 215, App	327	20	3	US-09-071-877-12	Sequence 12, Appl
255	35	100.0	16	4	US-08-474-349A-425	Sequence 425, App	328	20	3	US-08-484-223B-238	Sequence 238, App
256	35	100.0	16	4	US-09-315-304B-215	Sequence 215, App	329	20	3	US-08-554-616-59	Sequence 59, Appl
257	35	100.0	16	4	US-09-834-784-215	Sequence 215, App	330	20	3	US-09-082-279B-58	Sequence 58, Appl
258	35	100.0	16	4	US-09-515-965A-215	Sequence 215, App	331	20	3	US-09-082-279B-793	Sequence 793, App
259	35	100.0	16	4	US-09-515-965A-1668	Sequence 1668, App	332	20	3	US-09-045-520-8	Sequence 8, Appl
260	35	100.0	16	4	US-09-350-641C-215	Sequence 215, App	333	20	3	US-09-045-520-12	Sequence 12, Appl
261	35	100.0	17	1	US-08-073-028-56	Sequence 56, Appl	334	20	4	US-08-474-349A-422	Sequence 422, App
262	35	100.0	17	1	US-08-257-528B-61	Sequence 61, Appl	335	20	4	US-09-315-304B-58	Sequence 58, Appl
263	35	100.0	17	1	US-08-460-602A-61	Sequence 61, Appl	336	20	4	US-09-315-304B-793	Sequence 793, App
264	35	100.0	17	1	US-08-463-966A-61	Sequence 61, Appl	337	20	4	US-09-834-784-58	Sequence 58, Appl
265	35	100.0	17	1	US-08-465-217A-61	Sequence 61, Appl	338	20	4	US-09-834-784-793	Sequence 793, App
266	35	100.0	17	2	US-08-464-329A-61	Sequence 61, Appl	339	20	4	US-09-515-965A-58	Sequence 58, Appl
267	35	100.0	17	2	US-08-462-507A-61	Sequence 61, Appl	340	20	4	US-09-515-965A-793	Sequence 793, App
268	35	100.0	17	2	US-08-467-881A-61	Sequence 61, Appl	341	20	4	US-09-515-965A-1672	Sequence 1672, App
269	35	100.0	17	3	US-09-071-877-13	Sequence 13, Appl	342	20	4	US-09-350-641C-58	Sequence 58, Appl
270	35	100.0	17	3	US-08-554-616-56	Sequence 56, Appl	343	20	4	US-09-350-641C-793	Sequence 793, App
271	35	100.0	17	3	US-09-082-279B-214	Sequence 214, App	344	21	1	US-08-073-028-60	Sequence 60, Appl
272	35	100.0	17	3	US-09-045-920-13	Sequence 13, Appl	345	21	3	US-09-071-877-9	Sequence 9, Appl
273	35	100.0	17	4	US-08-474-349A-424	Sequence 424, App	346	21	3	US-08-554-616-60	Sequence 60, Appl
274	35	100.0	17	4	US-09-315-304B-214	Sequence 214, App	347	21	3	US-09-082-279B-1082	Sequence 1082, App
275	35	100.0	17	4	US-09-834-784-214	Sequence 214, App	348	21	3	US-09-082-279B-1083	Sequence 1083, App
276	35	100.0	17	4	US-09-515-965A-214	Sequence 214, App	349	21	3	US-09-082-279B-1362	Sequence 1362, App
277	35	100.0	17	4	US-09-515-965A-1669	Sequence 1669, App	350	21	3	US-09-045-520-9	Sequence 9, Appl
278	35	100.0	17	4	US-09-350-641C-214	Sequence 214, App	351	21	3	US-09-315-304B-1082	Sequence 1082, App
279	35	100.0	18	1	US-08-073-028-57	Sequence 57, Appl	352	21	4	US-09-315-304B-1083	Sequence 1083, App
280	35	100.0	18	1	US-08-257-528B-57	Sequence 57, Appl	353	21	4	US-09-315-304B-1362	Sequence 1362, App
281	35	100.0	18	1	US-08-460-602A-57	Sequence 57, Appl	354	21	4	US-09-315-304B-1363	Sequence 1363, App
282	35	100.0	18	1	US-08-463-966A-57	Sequence 57, Appl	355	21	4	US-09-834-784-1082	Sequence 1082, App
283	35	100.0	18	1	US-08-465-217A-57	Sequence 57, Appl	356	21	4	US-09-834-784-1083	Sequence 1083, App
284	35	100.0	18	2	US-08-464-329A-57	Sequence 57, Appl	357	21	4	US-09-834-784-1362	Sequence 1362, App
285	35	100.0	18	2	US-08-462-507A-57	Sequence 57, Appl	358	21	4	US-09-515-965A-1082	Sequence 1082, App
286	35	100.0	18	2	US-08-467-881A-57	Sequence 57, Appl	359	21	4	US-09-515-965A-1083	Sequence 1083, App
287	35	100.0	18	3	US-09-071-877-14	Sequence 14, App	360	21	4	US-09-515-965A-1362	Sequence 1362, App
288	35	100.0	18	3	US-08-554-616-57	Sequence 57, Appl	361	21	4	US-09-515-965A-1673	Sequence 1673, App
289	35	100.0	18	3	US-09-082-279B-3	Sequence 3, Appl	362	21	4	US-09-350-641C-1083	Sequence 1083, App
290	35	100.0	18	3	US-09-082-279B-57	Sequence 57, Appl	363	21	4	US-09-350-641C-1083	Sequence 1083, App
291	35	100.0	18	3	US-09-082-279B-98	Sequence 98, Appl	364	21	4	US-09-350-641C-1362	Sequence 1362, App
292	35	100.0	18	3	US-09-045-920-14	Sequence 14, App	365	22	1	US-08-073-028-61	Sequence 61, Appl
293	35	100.0	18	4	US-08-474-349A-423	Sequence 423, App	366	22	3	US-08-554-616-61	Sequence 61, Appl
294	35	100.0	18	4	US-09-315-304B-3	Sequence 3, Appl	367	22	4	US-09-515-965A-1674	Sequence 1674, App
295	35	100.0	18	4	US-09-315-304B-57	Sequence 57, Appl	368	23	1	US-08-073-028-62	Sequence 62, Appl
296	35	100.0	18	4	US-09-315-304B-98	Sequence 98, Appl	369	23	1	US-08-218-025A-152	Sequence 152, App
297	35	100.0	18	4	US-09-315-304B-1452	Sequence 1452, App	370	23	1	US-08-257-528B-67	Sequence 67, Appl
298	35	100.0	18	4	US-09-834-784-3	Sequence 3, Appl	371	23	1	US-08-460-602A-67	Sequence 67, Appl
299	35	100.0	18	4	US-09-834-784-57	Sequence 57, Appl	372	23	1	US-08-463-966A-67	Sequence 67, Appl
300	35	100.0	18	4	US-09-834-784-98	Sequence 98, Appl	373	23	1	US-08-465-217A-67	Sequence 67, Appl
301	35	100.0	18	4	US-09-515-965A-3	Sequence 3, Appl	374	23	2	US-08-464-329A-67	Sequence 67, Appl
302	35	100.0	18	4	US-09-515-965A-57	Sequence 57, Appl	375	23	2	US-08-462-507A-67	Sequence 67, Appl
303	35	100.0	18	4	US-09-515-965A-98	Sequence 98, Appl	376	23	2	US-08-467-881A-67	Sequence 67, Appl
304	35	100.0	18	4	US-09-515-965A-1452	Sequence 1452, App	377	23	3	US-08-484-223B-237	Sequence 237, App
305	35	100.0	18	4	US-09-515-965A-1670	Sequence 1670, App	378	23	3	US-08-554-616-62	Sequence 62, Appl
306	35	100.0	18	4	US-09-350-641C-3	Sequence 3, Appl	379	23	3	US-09-082-279B-59	Sequence 59, Appl
307	35	100.0	18	4	US-09-350-641C-57	Sequence 57, Appl	380	23	4	US-08-474-349A-421	Sequence 421, App
308	35	100.0	18	4	US-09-350-641C-98	Sequence 98, Appl	381	23	4	US-09-315-304B-59	Sequence 59, Appl
309	35	100.0	18	4	US-09-350-641C-1452	Sequence 1452, App	382	23	4	US-09-834-784-59	Sequence 59, Appl
310	35	100.0	19	1	US-08-073-028-58	Sequence 58, Appl	383	23	4	US-09-515-965A-59	Sequence 59, Appl
311	35	100.0	19	3	US-09-071-877-19	Sequence 19, Appl	384	23	4	US-09-515-965A-1675	Sequence 1675, App
312	35	100.0	19	3	US-08-554-616-58	Sequence 58, Appl	385	23	4	US-09-350-641C-59	Sequence 59, Appl
313	35	100.0	19	3	US-09-045-920-19	Sequence 19, Appl	386	24	1	US-08-073-028-63	Sequence 63, Appl
314	35	100.0	19	4	US-09-515-965A-1671	Sequence 1671, App	387	24	1	US-08-257-528B-65	Sequence 65, Appl
315	35	100.0	20	1	US-08-073-028-59	Sequence 59, Appl	388	24	1	US-08-460-602A-65	Sequence 65, Appl
316	35	100.0	20	1	US-08-218-025A-7	Sequence 7, Appl	389	24	1	US-08-463-966A-65	Sequence 65, Appl
317	35	100.0	20	1	US-08-218-025A-85	Sequence 85, Appl	390	24	1	US-08-465-217A-65	Sequence 65, Appl
318	35	100.0	20	1	US-08-218-025A-86	Sequence 86, Appl	391	24	2	US-08-464-329A-65	Sequence 65, Appl
319	35	100.0	20	1	US-08-257-528B-55	Sequence 55, Appl	392	24	2	US-08-462-507A-65	Sequence 65, Appl

393	35	100.0	24	2	US-08-467-881A-65	Sequence 65, Appl	466	35	100.0	28	4	US-08-470-896-161	Sequence 161, App
394	35	100.0	24	3	US-08-554-616-63	Sequence 63, Appl	467	35	100.0	28	4	US-08-470-896-162	Sequence 162, App
395	35	100.0	24	3	US-09-029-052-6	Sequence 6, Appl	468	35	100.0	28	4	US-08-485-546A-161	Sequence 161, App
396	35	100.0	24	3	US-09-082-279B-789	Sequence 789, App	469	35	100.0	28	4	US-08-485-546A-162	Sequence 162, App
397	35	100.0	24	3	US-09-082-279B-790	Sequence 790, App	470	35	100.0	28	4	US-09-834-784-231	Sequence 231, App
398	35	100.0	24	4	US-09-315-304B-789	Sequence 789, App	471	35	100.0	28	4	US-09-834-784-232	Sequence 232, App
399	35	100.0	24	4	US-09-315-304B-790	Sequence 790, App	472	35	100.0	28	4	US-09-834-784-377	Sequence 377, App
400	35	100.0	24	4	US-09-834-784-789	Sequence 789, App	473	35	100.0	28	4	US-09-834-784-380	Sequence 380, App
401	35	100.0	24	4	US-09-834-784-790	Sequence 790, App	474	35	100.0	28	4	US-09-515-965A-231	Sequence 231, App
402	35	100.0	24	4	US-09-515-965A-789	Sequence 789, App	475	35	100.0	28	4	US-09-515-965A-232	Sequence 232, App
403	35	100.0	24	4	US-09-515-965A-790	Sequence 790, App	476	35	100.0	28	4	US-09-515-965A-377	Sequence 377, App
404	35	100.0	24	4	US-09-515-965A-1676	Sequence 1676, App	477	35	100.0	28	4	US-09-515-965A-380	Sequence 380, App
405	35	100.0	24	4	US-09-350-641C-789	Sequence 789, App	478	35	100.0	28	4	US-09-515-965A-1680	Sequence 1680, App
406	35	100.0	24	4	US-09-350-641C-790	Sequence 790, App	479	35	100.0	28	4	US-09-350-641C-231	Sequence 231, App
407	35	100.0	25	1	US-08-073-028-64	Sequence 64, Appl	480	35	100.0	28	4	US-09-350-641C-232	Sequence 232, App
408	35	100.0	25	3	US-08-554-616-64	Sequence 64, Appl	481	35	100.0	28	4	US-09-350-641C-377	Sequence 377, App
409	35	100.0	25	4	US-09-515-965A-1677	Sequence 1677, App	482	35	100.0	28	4	US-09-350-641C-380	Sequence 380, App
410	35	100.0	26	1	US-08-073-028-65	Sequence 65, Appl	483	35	100.0	29	1	US-08-073-028-68	Sequence 68, Appl
411	35	100.0	26	1	US-08-257-528B-64	Sequence 64, Appl	484	35	100.0	29	3	US-08-554-616-68	Sequence 68, Appl
412	35	100.0	26	1	US-08-460-602A-64	Sequence 64, Appl	485	35	100.0	29	3	US-09-082-279B-635	Sequence 635, App
413	35	100.0	26	1	US-08-463-966A-64	Sequence 64, Appl	486	35	100.0	29	3	US-09-082-279B-637	Sequence 637, App
414	35	100.0	26	1	US-08-465-217A-64	Sequence 64, Appl	487	35	100.0	29	4	US-08-474-349A-419	Sequence 419, App
415	35	100.0	26	2	US-08-464-329A-64	Sequence 64, Appl	488	35	100.0	29	4	US-09-315-304B-635	Sequence 635, App
416	35	100.0	26	2	US-08-462-507A-64	Sequence 64, Appl	489	35	100.0	29	4	US-09-315-304B-637	Sequence 637, App
417	35	100.0	26	2	US-08-467-881A-64	Sequence 64, Appl	490	35	100.0	29	4	US-09-834-784-635	Sequence 635, App
418	35	100.0	26	3	US-08-484-223B-236	Sequence 236, App	491	35	100.0	29	4	US-09-834-784-637	Sequence 637, App
419	35	100.0	26	3	US-08-554-616-65	Sequence 65, Appl	492	35	100.0	29	4	US-09-515-965A-635	Sequence 635, App
420	35	100.0	26	3	US-08-082-279B-60	Sequence 60, Appl	493	35	100.0	29	4	US-09-515-965A-637	Sequence 637, App
421	35	100.0	26	4	US-08-474-349A-420	Sequence 420, App	494	35	100.0	29	4	US-09-515-965A-1681	Sequence 1681, App
422	35	100.0	26	4	US-09-315-304B-60	Sequence 60, Appl	495	35	100.0	29	4	US-09-350-641C-635	Sequence 635, App
423	35	100.0	26	4	US-09-834-784-60	Sequence 60, Appl	496	35	100.0	29	4	US-09-350-641C-637	Sequence 637, App
424	35	100.0	26	4	US-09-515-965A-60	Sequence 60, Appl	497	35	100.0	30	1	US-08-073-028-16	Sequence 16, Appl
425	35	100.0	26	4	US-09-515-965A-1678	Sequence 1678, App	498	35	100.0	30	1	US-08-073-028-69	Sequence 69, Appl
426	35	100.0	26	4	US-09-350-641C-60	Sequence 60, Appl	499	35	100.0	30	1	US-08-257-528B-58	Sequence 58, Appl
427	35	100.0	27	1	US-08-073-028-66	Sequence 66, Appl	500	35	100.0	30	1	US-08-257-528B-62	Sequence 62, Appl
428	35	100.0	27	1	US-08-257-528B-63	Sequence 63, Appl							
429	35	100.0	27	1	US-08-460-602A-63	Sequence 63, Appl							
430	35	100.0	27	1	US-08-463-966A-63	Sequence 63, Appl							
431	35	100.0	27	1	US-08-465-217A-63	Sequence 63, Appl							
432	35	100.0	27	2	US-08-464-329A-63	Sequence 63, Appl							
433	35	100.0	27	2	US-08-462-507A-63	Sequence 63, Appl							
434	35	100.0	27	2	US-08-467-881A-63	Sequence 63, Appl							
435	35	100.0	27	3	US-08-554-616-66	Sequence 66, Appl							
436	35	100.0	27	4	US-09-515-965A-1679	Sequence 1679, App							
437	35	100.0	28	1	US-08-073-028-67	Sequence 67, Appl							
438	35	100.0	28	3	US-08-486-099-161	Sequence 161, App							
439	35	100.0	28	3	US-08-486-099-162	Sequence 162, App							
440	35	100.0	28	3	US-08-484-223B-161	Sequence 161, App							
441	35	100.0	28	3	US-08-484-223B-162	Sequence 162, App							
442	35	100.0	28	3	US-08-919-597-161	Sequence 161, App							
443	35	100.0	28	3	US-08-919-597-162	Sequence 162, App							
444	35	100.0	28	3	US-08-475-668A-161	Sequence 161, App							
445	35	100.0	28	3	US-08-475-668A-162	Sequence 162, App							
446	35	100.0	28	3	US-08-485-551A-161	Sequence 161, App							
447	35	100.0	28	3	US-08-485-551A-162	Sequence 162, App							
448	35	100.0	28	3	US-08-471-913A-161	Sequence 161, App							
449	35	100.0	28	3	US-08-471-913A-162	Sequence 162, App							
450	35	100.0	28	3	US-08-554-616-67	Sequence 67, Appl							
451	35	100.0	28	3	US-08-485-264A-161	Sequence 161, App							
452	35	100.0	28	3	US-08-485-264A-162	Sequence 162, App							
453	35	100.0	28	3	US-09-082-279B-231	Sequence 231, App							
454	35	100.0	28	3	US-09-082-279B-232	Sequence 232, App							
455	35	100.0	28	3	US-09-082-279B-377	Sequence 377, App							
456	35	100.0	28	3	US-09-082-279B-380	Sequence 380, App							
457	35	100.0	28	4	US-08-474-349A-161	Sequence 161, App							
458	35	100.0	28	4	US-08-474-349A-162	Sequence 162, App							
459	35	100.0	28	4	US-08-474-349A-429	Sequence 429, App							
460	35	100.0	28	4	US-09-315-304B-231	Sequence 231, App							
461	35	100.0	28	4	US-09-315-304B-232	Sequence 232, App							
462	35	100.0	28	4	US-09-315-304B-377	Sequence 377, App							
463	35	100.0	28	4	US-09-315-304B-380	Sequence 380, App							
464	35	100.0	28	4	US-08-973-952-14	Sequence 14, Appl							
465	35	100.0	28	4	US-08-973-952-15	Sequence 15, Appl							

RESULT 1
US-08-257-528B-69
; Patent No. 5639854
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,528B
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-336 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163

ALIGNMENTS

; INFORMATION FOR SEQ ID NO: 69:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-257-528B-69

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 2

US-08-361-479-1

; Sequence 1, Application US/08361479
; Patent No. 5693752

; GENERAL INFORMATION:

; APPLICANT: KATINGER, HERMAN; RUEKER, FLORIAN; HIMMLER,

; APPLICANT: GOTTFRIED; MUSTER, THOMAS; TRKOLA, ALEXANDRA; PURTSCHER, MARTIN; MAIWAL

; APPLICANT: GEORG; STEINDL, FRANZ

; TITLE OF INVENTION: PEPTIDES THAT INDUCE ANTIBODIES WHICH

; TITLE OF INVENTION: NEUTRALIZE GENTICALLY DIVERGENT HIV-1 ISOLATES.

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN & MUSERLIAN

; STREET: 600 THIRD AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/361,479

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/932,787

; FILING DATE: 29-AUG-1992

; APPLICATION NUMBER: A 987/92

; FILING DATE: 14-MAY-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 366.015

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-661-8000

; TELEFAX: 212-661-8002

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6

; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: UNKNOWN

; MOLECULE TYPE:

; DESCRIPTION: PEPTIDE

; HYPOTHETICAL: No

; ORIGINAL SOURCE:

; ORGANISM: HIV-1

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

; DEVELOPMENTAL STAGE:

; HAPLOTYPE:

; TISSUE TYPE:

; CELL TYPE:

; INDIVIDUAL ISOLATE: BH10

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

; CELL LINE:

; ORGANELLE:

; FEATURE:

; NAME/KEY: GP160 FRAGMENT

; LOCATION: RESIDUE 662 TO 667

; IDENTIFICATION METHOD:

; OTHER INFORMATION: EPIOTOPE OF HUMAN MONOCLONAL ANTIBODY

; OTHER INFORMATION: DIRECTED AGAINST HIV-1 GP160

US-08-361-479-1

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 3

US-08-473-576-1

; Sequence 1, Application US/08473576

; Patent No. 5756674

; GENERAL INFORMATION:

; APPLICANT: KATINGER, HERMAN; RUEKER, FLORIAN; HIMMLER,

; APPLICANT: GOTTFRIED; MUSTER, THOMAS; TRKOLA, ALEXANDRA; PURTSCHER, MARTIN; MAIWAL

; APPLICANT: GEORG; STEINDL, FRANZ

; TITLE OF INVENTION: PEPTIDES THAT INDUCE ANTIBODIES WHICH

; TITLE OF INVENTION: NEUTRALIZE GENTICALLY DIVERGENT HIV-1 ISOLATES.

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN & MUSERLIAN

; STREET: 600 THIRD AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/473,576

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/361,479

; FILING DATE: 22-DEC-1994

; APPLICATION NUMBER: 07/932,787

; FILING DATE: 29-AUG-1992

; APPLICATION NUMBER: A 987/92

; FILING DATE: 14-MAY-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 366.015

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-661-8000

; TELEFAX: 212-661-8002

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6

; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: UNKNOWN

; MOLECULE TYPE:

; DESCRIPTION: PEPTIDE

; HYPOTHETICAL: No

; ORIGINAL SOURCE:

; ORGANISM: HIV-1

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

DEVELOPMENTAL STAGE:

HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY: GP160 FRAGMENT
LOCATION: RESIDUE 662 TO 667
IDENTIFICATION METHOD:
OTHER INFORMATION: EPITOPE OF HUMAN MONOCLONAL ANTIBODY
OTHER INFORMATION: DIRECTED AGAINST HIV-1 GP160
US-08-473-576-1

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 4

US-08-460-602A-69
Sequence 69, Application US/08460602A
Patent No. 5759769
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460.602A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-450 MIS:jfb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-460-602A-69

Query Match 100.0%; Score 35; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 5

US-08-323-192D-47
Sequence 47, Application US/08323192D
Patent No. 5786199
GENERAL INFORMATION:
APPLICANT: Palese, Peter
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,192D
FILING DATE: 14-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-323-192D-47

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 6

US-08-463-966A-69
Sequence 69, Application US/08463966A
Patent No. 5795955
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto

STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463.966A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-966A-69

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 7
US-08-465-217A-69
Sequence 69, Application US/08465217A
Patent No. 580822
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465.217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-217A-69

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 8
US-08-464-329A-69
Sequence 69, Application US/08464329A
Patent No. 581754
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,329A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids

```
;
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;
US-08-464-329A-69
;
Query Match      100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      1 ELDKWA 6

RESULT 9
US-08-021-879-1
; Sequence 1, Application US/08021879
; Patent No. 5817767
; GENERAL INFORMATION:
; APPLICANT: Graham P. Allaway
; APPLICANT: Paul J. Maddon
; TITLE OF INVENTION: SYNERGISTIC COMPOSITION OF CD4-BASED
; TITLE OF INVENTION: PROTEIN AND ANTI-HIV-1 ANTIBODY, AND
; TITLE OF INVENTION: METHODS OF USING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021,879
; FILING DATE: 24-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41189/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOPUI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-021-879-1
Query Match      100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      1 ELDKWA 6

RESULT 10
US-08-470-887A-46
; Sequence 46, Application US/08470887A
; Patent No. 5820871
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,508B
; FILING DATE: 01-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
```

```
;
;      TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
;      TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
;      NUMBER OF SEQUENCES: 60
;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Pennie & Edmonds
;      STREET: 1155 Avenue of the Americas
;      CITY: New York
;      STATE: New York
;      COUNTRY: USA
;      ZIP: 10036-2711
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/470,887A
;      FILING DATE: 06-JUN-1995
;      CLASSIFICATION:
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Coruzzi, Laura A.
;      REGISTRATION NUMBER: 30,742
;      REFERENCE/DOCKET NUMBER: 7682-036
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) 790-9090
;      TELEFAX: (212) 869-9741/8864
;      TELEX: 66141 PENNIE
;      INFORMATION FOR SEQ ID NO: 46:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 6 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: single
;      TOPOLOGY: unknown
;      MOLECULE TYPE: peptide
;
US-08-470-887A-46
Query Match      100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      1 ELDKWA 6

RESULT 11
US-08-252-508B-46
; Sequence 46, Application US/08252508B
; Patent No. 5854037
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,508B
; FILING DATE: 01-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
```

; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7882-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-252-508B-46

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 12

US-08-975-699-23
; Sequence 23, Application US/08975699
; Patent No. 5858369

; GENERAL INFORMATION:
; APPLICANT: MATSUO, KAZUHIRO
; APPLICANT: CHUJO, YOSHITOMO
; APPLICANT: YAMAZAKI, AKIHIRO
; APPLICANT: HONDA, MITSUO
; APPLICANT: YAMAKAZI, SHUDO
; APPLICANT: TASAKA, HIROMICHI
; TITLE OF INVENTION: ANTI-AIDS SECRETORY RECOMBINANT BCG
; TITLE OF INVENTION: VACCINE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; STREET: ARLINGTON
; CITY: VA
; STATE: USA
; COUNTRY: 22202
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,699
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/619,512
; FILING DATE: 29-MAR-1996
; APPLICATION NUMBER: PCT/JP95/01515
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 178462/1994
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN P.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-795-0X PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; STRAIN: HIV-1
; US-08-975-699-23

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 13

US-08-417-210A-147
; Sequence 147, Application US/08417210A
; Patent No. 5863542

; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,210A
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454310-2690
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-840-3333
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; US-08-417-210A-147

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 14

US-08-843-718-1
; Sequence 1, Application US/08843718
; Patent No. 5866694
; GENERAL INFORMATION:

APPLICANT: KATINGER, HERMAN; RUEKER, FLORIAN; HIMMLER,
APPLICANT: GOTTFRIED; MUSTER, THOMAS; TRKOLA, ALEXANDRA; PURTSCHER, MARTIN; MAIWAL
APPLICANT: GEORG; STEINDL, FRANZ
TITLE OF INVENTION: PEPTIDES THAT INDUCE ANTIBODIES WHICH
TITLE OF INVENTION: NEUTRALIZE GENTICALLY DIVERGENT HIV-1 ISOLATES.
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,718
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/932,787
FILING DATE: 29-AUG-1992
APPLICATION NUMBER: A 987/92
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 366.015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-661-8000
TELEFAX: 212-661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HIV-1
STRAIN:
INDIVIDUAL ISOLATE: BH10
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY: GP160 FRAGMENT
LOCATION: RESIDUE 662 TO 667
IDENTIFICATION METHOD:
OTHER INFORMATION: EPITOPE OF HUMAN MONOCLONAL ANTIBODY
OTHER INFORMATION: DIRECTED AGAINST HIV-1 GP160
US-08-843-718-1
Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 1 ELDKWA 6
RESULT 15
US-08-462-507A-69
; Sequence 69, Application US/08462507A

Patent No. 5876731
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,507A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-451 MTS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-462-507A-69
Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 1 ELDKWA 6
RESULT 16
US-08-972-089-23
; Sequence 23, Application US/08972089
; Patent No. 5885580
GENERAL INFORMATION:
APPLICANT: MATSUO, KAZUHIRO
APPLICANT: CHUJO, YOSHITOMO
APPLICANT: YAMAZAKI, AKIHIRO
APPLICANT: HONDA, MITSUO
APPLICANT: YAMAKAZI, SHUDO
APPLICANT: TASAKA, HIROMICHI
TITLE OF INVENTION: ANTI-AIDS SECRETORY RECOMBINANT BCG
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972.089
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975.699
FILING DATE:
APPLICATION NUMBER: PCT/JP95/01515
FILING DATE: 31-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 178462/1994
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-795-0X PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
STRAIN: HIV-1
US-08-972-089-23

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 17
US-08-467-881A-69
Sequence 69, Application US/08467881A
Patent No. 5951986
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467.881A

FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-488 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-881A-69

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 18
US-09-106-377-46
Sequence 46, Application US/09106377
Patent No. 6001634
GENERAL INFORMATION:
APPLICANT: Palese, Peter
APPLICANT: Garcia-Sastre, Adolfo
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,377
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/252,508
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:

;
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-106-377-46

Query Match 100.0%; Score 35; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 19

US-09-124-900-11
; Sequence 11, Application US/09124900
; Patent No. 6268484

GENERAL INFORMATION:

; APPLICANT: KATINGER, Hermann
; APPLICANT: BUCHACHER, Andrea
; APPLICANT: ERNST, Wolfgang
; APPLICANT: BALLAUN, Claudia
; APPLICANT: PURTSCHER, Martin
; APPLICANT: TRKOLA, Alexandra
; APPLICANT: FREDL, Renate
; APPLICANT: SCHMATZ, Christine
; APPLICANT: KLIMA, Annelies
; APPLICANT: STEINDL, Franz
; APPLICANT: MUSTER, Thomas
; TITLE OF INVENTION: HIV-Vaccines

; FILE REFERENCE: 1939-112P
; CURRENT APPLICATION NUMBER: US/09/124,900
; CURRENT FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: PCT/EP95/01481
; PRIOR FILING DATE: 1995-04-19

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1
US-09-124-900-11

Query Match 100.0%; Score 35; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 20

US-09-340-798A-53
; Sequence 53, Application US/09340798A
; Patent No. 6534312

GENERAL INFORMATION:

; APPLICANT: SHIVER, JOHN W.
; LIU, MARGARET A.
; PERRY, HELEN C.
; DAVIES, MARY-ELLEN M.
; FREED, DANIEL C.

; TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: US

ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,798A
FILING DATE: 28-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/877,418
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19729Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720

INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 53:

US-09-340-798A-53
Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 21

US-09-136-159A-147
; Sequence 147, Application US/09136159A
; Patent No. 6596279

GENERAL INFORMATION:

; APPLICANT: Virogenetics Corporation
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I
; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
; FILE REFERENCE: 454310-2690.1
; CURRENT APPLICATION NUMBER: US/09/136,159A
; CURRENT FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: US 08/417,210
; PRIOR FILING DATE: 1995-04-05
; PRIOR APPLICATION NUMBER: US 08/223,842
; PRIOR FILING DATE: 1994-04-06
; PRIOR APPLICATION NUMBER: US 07/897,382
; PRIOR FILING DATE: 1992-06-11
; PRIOR APPLICATION NUMBER: US 07/715,921
; PRIOR FILING DATE: 1991-06-14
; PRIOR APPLICATION NUMBER: US 08/105,483
; PRIOR FILING DATE: 1993-08-12
; PRIOR APPLICATION NUMBER: US 07/847,951
; PRIOR FILING DATE: 1992-03-06
; PRIOR APPLICATION NUMBER: US 07/713,967
; PRIOR FILING DATE: 1991-06-11
; PRIOR APPLICATION NUMBER: US 07/666,056
; PRIOR FILING DATE: 1991-03-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 147
; LENGTH: 6
; TYPE: PRT

```
; ORGANISM: Human immunodeficiency virus type 1
US-09-136-159A-147

Query Match      100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      1 ELDKWA 6
      |||||
      1 ELDKWA 6

RESULT 22
US-09-525-874-1
; Sequence 1, Application US/09525874
; Patent No. 6596497
; GENERAL INFORMATION:
; APPLICANT: Jiang, Shibo
; APPLICANT: Debnath, Asim K.
; TITLE OF INVENTION: Screening of Antiviral Compounds
; TITLE OF INVENTION: Targeted to the HIV-1 gp41 Core Structure
; FILE REFERENCE: 990006/RSB
; CURRENT APPLICATION NUMBER: US/09/525,874
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: US 60/124,907
; EARLIER FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Epitope recognized by human MAb 2F5
; FEATURE:
; LOCATION: 662..667
US-09-525-874-1

Query Match      100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      1 ELDKWA 6
      |||||
      1 ELDKWA 6

RESULT 23
US-09-873-459A-4
; Sequence 4, Application US/09873459A
; Patent No. 6627202
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HEV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-873-459A-4

Query Match      100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
      |||||
      1 ELDKWA 6

; ORGANISM: Human immunodeficiency virus type 1
US-09-136-159A-147

Query Match      100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      1 ELDKWA 6
      |||||
      1 ELDKWA 6

RESULT 24
US-08-257-528B-98
; Sequence 98, Application US/08257528B
; Patent No. 5639854
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,528B
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-336 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-257-528B-98

Query Match      100.0%; Score 35; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      1 ELDKWA 6
      |||||
      1 ELDKWA 6

RESULT 25
US-08-460-602A-98
; Sequence 98, Application US/08460602A
; Patent No. 5759769
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/460,602A
APPLICATION NUMBER: 1038-487 MIS:jb
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-450 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-460-602A-98

Query Match 100.0%; Score 35; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 26
US-08-463-966A-98
Sequence 98, Application US/08463966A
Patent No. 5795955
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,966A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:

NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-966A-98

Query Match 100.0%; Score 35; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 27
US-08-465-217A-98
Sequence 98, Application US/08465217A
Patent No. 5800822
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-217A-98

Query Match 100.0%; Score 35; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 28

US-08-464-329A-98
; Sequence 98, Application US/08464329A
; Patent No. 5817754
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464.329A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-464-329A-98

Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Mismatches 0; Conservative 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 29

US-08-462-507A-98
; Sequence 98, Application US/08462507A
; Patent No. 5876731
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele

; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,507A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-451 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-462-507A-98

Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Mismatches 6; Conservative 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 30

US-08-776-585-17
; Sequence 17, Application US/08776585
; Patent No. 5932426
; GENERAL INFORMATION:
; APPLICANT: BARALLE, Francesco E.
; APPLICANT: SCODELLER, Eduardo
; APPLICANT: TISMINETSKY, Sergio
; TITLE OF INVENTION: MOLECULAR PRESENTING SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,585
; FILING DATE: 31-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/03114
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 69582/106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-776-585-17

Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 31
US-08-467-881A-98
; Sequence 98, Application US/08467881A
; Patent No. 5951986
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,881A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-488 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-467-881A-98

Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 32
US-09-289-942A-1
; Sequence 1, Application US/09289942A
; Patent No. 6482928
; GENERAL INFORMATION:
; APPLICANT: Pai, Emil F.
; APPLICANT: Klein, Michel H.
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Arthur
; TITLE OF INVENTION: Fab'-EPI TOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5
; FILE REFERENCE: 1038-926 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/289,942A
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; US-09-289-942A-1

Query Match 100.0%; Score 35; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 33
US-09-873-459A-2
; Sequence 2, Application US/09873459A
; Patent No. 6627202
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-09-873-459A-2

Query Match 100.0%; Score 35; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 34

US-08-073-028-51
; Sequence 51, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073.028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-073-028-51

Query Match 100.0%; Score 35; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 35

US-09-071-877-15
; Sequence 15, Application US/09071877
; Patent No. 6015881
; GENERAL INFORMATION:
; APPLICANT: Kang, Myung-Chol
; APPLICANT: Bray, Brian
; APPLICANT: Lichty, Maynard
; APPLICANT: Mader, Catherine
; APPLICANT: Merutka, Gene
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS
; FILE REFERENCE: 7872-050
; CURRENT APPLICATION NUMBER: US/09/071.877
; CURRENT FILING DATE: 1998-05-01

; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: fragment
US-09-071-877-15

Query Match 100.0%; Score 35; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 2 ELDKWA 7

RESULT 36

US-08-554-616-51
; Sequence 51, Application US/08554616
; Patent No. 6133418
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,616
; FILING DATE: 06-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/073,028
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-554-616-51

Query Match 100.0%; Score 35; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 39
US-08-474-349A-434
: Sequence 434: Application IIS/08474349A

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 219
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-219

Query Match 100.0%; Score 35; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 41

US-09-834-784-219
; Sequence 219, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 219
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-219

Query Match 100.0%; Score 35; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 42

US-09-515-965A-219
; Sequence 219, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 219
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-219

Query Match 100.0%; Score 35; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 43

US-09-515-965A-1664
; Sequence 1664, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1664
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-1664

Query Match 100.0%; Score 35; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 44

US-09-350-641C-219
; Sequence 219, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304

; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 05/082,279
 ; PRIOR FILING DATE: 1998-05-20
 ; NUMBER OF SEQ ID NOS: 1757
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 219
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Core polypeptide
 US-09-350-641C-219

Query Match 100.0%; Score 35; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 45
 US-08-073-028-52
 ; Sequence 52, Application US/08073028
 ; Patent No. 5464933
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/073,028
 ; FILING DATE: 07-JUN-1993
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7872-004-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 52:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 US-08-073-028-52

Query Match 100.0%; Score 35; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 2 ELDKWA 7

RESULT 46
 US-08-975-699-13
 ; Sequence 13, Application US/08975699
 ; Patent No. 5858369
 ; GENERAL INFORMATION:
 ; APPLICANT: MATSUO, KAZUHIRO
 ; APPLICANT: CHUJO, YOSHITOMO
 ; APPLICANT: YAMAZAKI, AKIHIRO
 ; APPLICANT: HONDA, MITSUO
 ; APPLICANT: YAMAKAZI, SHUDO
 ; APPLICANT: TASAKA, HIROMICHI
 ; TITLE OF INVENTION: ANTI-AIDS SECRETORY RECOMBINANT BCG
 ; TITLE OF INVENTION: VACCINE
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/975,699
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/619,512
 ; FILING DATE: 29-MAR-1996
 ; APPLICATION NUMBER: PCT/JP95/01515
 ; FILING DATE: 31-JUL-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 178462/1994
 ; FILING DATE: 29-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 10-795-0X PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 ; STRAIN: HIV-1
 US-08-975-699-13

Query Match 100.0%; Score 35; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 8 ELDKWA 13

RESULT 47
 US-08-972-089-13
 ; Sequence 13, Application US/08972089
 ; Patent No. 5885580
 ; GENERAL INFORMATION:

APPLICANT: MATSUO, KAZUHIRO
APPLICANT: CHUJO, YOSHITOMO
APPLICANT: YAMAZAKI, AKIHIRO
APPLICANT: HONDA, MITSUO
APPLICANT: YAMAKAZI, SHUO
APPLICANT: TASAKA, HIROMICHI
TITLE OF INVENTION: ANTI-AIDS SECRETORY RECOMBINANT BCG
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,089
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/975,699
FILING DATE:
APPLICATION NUMBER: PCT/JP95/01515
FILING DATE: 31-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 178462/1994
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-795-0X PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
STRAIN: HIV-1
US-08-972-089-13

Query Match 100.0%; Score 35; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 8 ELDKWA 13

RESULT 48
US-08-486-099-169
Sequence 169, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-099-169

Query Match 100.0%; Score 35; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7

RESULT 49
US-08-486-099-170
Sequence 170, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-486-099-170

Query Match 100.0%; Score 35; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7

; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-486-099-171

Query Match 100.0%; Score 35; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7

Search completed: March 16, 2004, 09:18:48
Job time : 25 secs

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2004, 09:16:31 ; Search time 34 Seconds
(without alignments)
37.262 Million cell updates/sec

Title: US-10-024-329-2

Perfect score: 35

Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	6	9	US-09-873-459A-4
2	35	100.0	6	14	US-10-041-414-7
3	35	100.0	6	14	US-10-024-329-2
4	35	100.0	6	14	US-10-448-546-4
5	35	100.0	6	15	US-10-283-403-12
6	35	100.0	6	15	US-10-369-121-53
7	35	100.0	7	9	US-09-873-459A-2
8	35	100.0	7	14	US-10-448-546-2
9	35	100.0	10	10	US-09-931-325A-132
10	35	100.0	10	10	US-09-930-915A-173
11	35	100.0	10	14	US-10-200-708-31
12	35	100.0	10	14	US-10-200-708-404
13	35	100.0	10	14	US-10-200-708-456
14	35	100.0	10	14	US-10-200-708-477
15	35	100.0	12	14	US-10-351-641-219

16	35	100.0	12	15	US-10-005-305-43	Sequence 43, Appl
17	35	100.0	12	15	US-10-005-305-88	Sequence 88, Appl
18	35	100.0	13	14	US-10-252-136-22	Sequence 22, Appl
19	35	100.0	13	14	US-10-252-136-23	Sequence 23, Appl
20	35	100.0	13	14	US-10-252-136-24	Sequence 24, Appl
21	35	100.0	13	14	US-10-252-136-25	Sequence 25, Appl
22	35	100.0	13	14	US-10-252-136-26	Sequence 26, Appl
23	35	100.0	13	14	US-10-351-641-218	Sequence 218, App
24	35	100.0	13	14	US-10-351-641-267	Sequence 267, App
25	35	100.0	13	14	US-10-351-641-268	Sequence 268, App
26	35	100.0	13	14	US-10-351-641-269	Sequence 269, App
27	35	100.0	13	14	US-10-351-641-270	Sequence 270, App
28	35	100.0	13	14	US-10-351-641-530	Sequence 530, App
29	35	100.0	13	14	US-10-351-641-531	Sequence 531, App
30	35	100.0	13	15	US-10-005-305-44	Sequence 44, Appl
31	35	100.0	13	15	US-10-005-305-87	Sequence 87, Appl
32	35	100.0	14	10	US-09-931-325A-133	Sequence 133, App
33	35	100.0	14	10	US-09-930-915A-174	Sequence 174, App
34	35	100.0	14	14	US-10-351-641-217	Sequence 217, App
35	35	100.0	14	14	US-10-351-641-229	Sequence 229, App
36	35	100.0	14	15	US-10-005-305-45	Sequence 45, Appl
37	35	100.0	14	15	US-10-005-305-86	Sequence 86, Appl
38	35	100.0	15	9	US-09-810-310-41	Sequence 41, Appl
39	35	100.0	15	14	US-10-252-136-19	Sequence 19, Appl
40	35	100.0	15	14	US-10-252-136-20	Sequence 20, Appl
41	35	100.0	15	14	US-10-252-136-21	Sequence 21, Appl
42	35	100.0	15	14	US-10-351-641-216	Sequence 216, App
43	35	100.0	15	14	US-10-351-641-372	Sequence 372, App
44	35	100.0	15	14	US-10-351-641-373	Sequence 373, App
45	35	100.0	15	14	US-10-351-641-374	Sequence 374, App
46	35	100.0	15	14	US-10-351-641-513	Sequence 513, App
47	35	100.0	15	14	US-10-351-641-514	Sequence 514, App
48	35	100.0	15	14	US-10-351-641-515	Sequence 515, App
49	35	100.0	15	14	US-10-351-641-792	Sequence 792, App
50	35	100.0	15	15	US-10-005-305-46	Sequence 46, Appl
51	35	100.0	15	15	US-10-005-305-85	Sequence 85, Appl
52	35	100.0	16	14	US-10-351-641-215	Sequence 215, App
53	35	100.0	16	15	US-10-005-305-47	Sequence 47, Appl
54	35	100.0	16	15	US-10-005-305-84	Sequence 84, Appl
55	35	100.0	17	14	US-10-351-641-214	Sequence 214, App
56	35	100.0	17	15	US-10-005-305-48	Sequence 48, Appl
57	35	100.0	17	15	US-10-005-305-83	Sequence 83, Appl
58	35	100.0	18	14	US-10-351-641-3	Sequence 3, Appl
59	35	100.0	18	14	US-10-351-641-57	Sequence 57, Appl
60	35	100.0	18	14	US-10-351-641-98	Sequence 98, Appl
61	35	100.0	18	14	US-10-351-641-1452	Sequence 1452, Ap
62	35	100.0	18	15	US-10-005-305-49	Sequence 49, Appl
63	35	100.0	18	15	US-10-005-305-82	Sequence 82, Appl
64	35	100.0	19	15	US-10-005-305-50	Sequence 50, Appl
65	35	100.0	19	15	US-10-005-305-81	Sequence 81, Appl
66	35	100.0	20	14	US-10-351-641-58	Sequence 58, Appl
67	35	100.0	20	14	US-10-351-641-793	Sequence 793, App
68	35	100.0	20	15	US-10-005-305-51	Sequence 51, Appl
69	35	100.0	20	15	US-10-005-305-80	Sequence 80, Appl
70	35	100.0	21	14	US-10-351-641-1083	Sequence 1082, Ap
71	35	100.0	21	14	US-10-351-641-1083	Sequence 1083, Ap
72	35	100.0	21	14	US-10-351-641-1362	Sequence 1362, Ap
73	35	100.0	21	15	US-10-005-305-52	Sequence 52, Appl
74	35	100.0	21	15	US-10-005-305-79	Sequence 79, Appl
75	35	100.0	22	15	US-10-005-305-53	Sequence 53, Appl
76	35	100.0	22	15	US-10-005-305-78	Sequence 78, Appl
77	35	100.0	23	14	US-10-351-641-59	Sequence 59, Appl
78	35	100.0	23	15	US-10-005-305-54	Sequence 54, Appl
79	35	100.0	23	15	US-10-005-305-77	Sequence 77, Appl
80	35	100.0	24	14	US-10-351-641-789	Sequence 789, App
81	35	100.0	24	14	US-10-351-641-790	Sequence 790, App
82	35	100.0	24	15	US-10-005-305-55	Sequence 55, Appl
83	35	100.0	24	15	US-10-005-305-76	Sequence 76, Appl
84	35	100.0	24	15	US-10-005-305-201	Sequence 201, App
85	35	100.0	25	15	US-10-005-305-56	Sequence 56, Appl
86	35	100.0	25	15	US-10-005-305-75	Sequence 75, Appl
87	35	100.0	26	14	US-10-351-641-60	Sequence 60, Appl
88	35	100.0	26	15	US-10-005-305-57	Sequence 57, Appl

89	35	100.0	26	15	US-10-005-305-74	Sequence 74, Appl	162	35	100.0	36	14	US-10-252-136-3	Sequence 3, Appl
90	35	100.0	27	15	US-10-005-305-58	Sequence 58, Appl	163	35	100.0	36	14	US-10-252-136-4	Sequence 4, Appl
91	35	100.0	27	15	US-10-005-305-73	Sequence 73, Appl	164	35	100.0	36	14	US-10-252-136-5	Sequence 5, Appl
92	35	100.0	28	14	US-10-252-136-14	Sequence 14, Appl	165	35	100.0	36	14	US-10-252-136-31	Sequence 31, Appl
93	35	100.0	28	14	US-10-252-136-15	Sequence 15, Appl	166	35	100.0	36	14	US-10-252-136-32	Sequence 32, Appl
94	35	100.0	28	14	US-10-351-641-231	Sequence 231, Appl	167	35	100.0	36	14	US-10-252-136-33	Sequence 33, Appl
95	35	100.0	28	14	US-10-351-641-232	Sequence 232, Appl	168	35	100.0	36	14	US-10-252-136-36	Sequence 36, Appl
96	35	100.0	28	14	US-10-351-641-377	Sequence 377, Appl	169	35	100.0	36	14	US-10-252-136-37	Sequence 37, Appl
97	35	100.0	28	14	US-10-351-641-380	Sequence 380, Appl	170	35	100.0	36	14	US-10-252-136-39	Sequence 39, Appl
98	35	100.0	28	15	US-10-005-305-59	Sequence 59, Appl	171	35	100.0	36	14	US-10-252-136-40	Sequence 40, Appl
99	35	100.0	28	15	US-10-005-305-72	Sequence 72, Appl	172	35	100.0	36	14	US-10-252-136-42	Sequence 42, Appl
100	35	100.0	29	14	US-10-005-305-61	Sequence 61, Appl	173	35	100.0	36	14	US-10-252-136-43	Sequence 43, Appl
101	35	100.0	29	14	US-10-351-641-635	Sequence 635, Appl	174	35	100.0	36	14	US-10-252-136-44	Sequence 44, Appl
102	35	100.0	29	15	US-10-351-641-637	Sequence 60, Appl	175	35	100.0	36	14	US-10-252-136-45	Sequence 45, Appl
103	35	100.0	29	15	US-10-005-305-60	Sequence 70, Appl	176	35	100.0	36	14	US-10-252-136-46	Sequence 46, Appl
104	35	100.0	29	15	US-10-005-305-71	Sequence 200, Appl	177	35	100.0	36	14	US-10-252-136-47	Sequence 47, Appl
105	35	100.0	30	14	US-10-005-305-200	Sequence 18, Appl	178	35	100.0	36	14	US-10-252-136-50	Sequence 50, Appl
106	35	100.0	30	14	US-10-252-136-18	Sequence 600, Appl	179	35	100.0	36	14	US-10-252-136-51	Sequence 51, Appl
107	35	100.0	30	14	US-10-351-641-600	Sequence 600, Appl	180	35	100.0	36	14	US-10-252-136-56	Sequence 56, Appl
108	35	100.0	30	14	US-10-351-641-794	Sequence 794, Appl	181	35	100.0	36	14	US-10-252-136-57	Sequence 57, Appl
109	35	100.0	30	15	US-10-351-641-907	Sequence 907, Appl	182	35	100.0	36	14	US-10-252-136-58	Sequence 58, Appl
110	35	100.0	30	15	US-10-005-305-28	Sequence 28, Appl	183	35	100.0	36	14	US-10-252-136-59	Sequence 59, Appl
111	35	100.0	30	15	US-10-005-305-61	Sequence 61, Appl	184	35	100.0	36	14	US-10-252-136-60	Sequence 60, Appl
112	35	100.0	31	14	US-10-005-305-70	Sequence 70, Appl	185	35	100.0	36	14	US-10-252-136-61	Sequence 61, Appl
113	35	100.0	31	14	US-10-351-641-744	Sequence 744, Appl	186	35	100.0	36	14	US-10-252-136-62	Sequence 62, Appl
114	35	100.0	31	14	US-10-351-641-923	Sequence 923, Appl	187	35	100.0	36	14	US-10-158-742A-8	Sequence 8, Appl
115	35	100.0	31	15	US-10-005-305-29	Sequence 29, Appl	188	35	100.0	36	14	US-10-323-314-8	Sequence 7, Appl
116	35	100.0	31	15	US-10-005-305-62	Sequence 62, Appl	189	35	100.0	36	14	US-10-278-364A-7	Sequence 209, Appl
117	35	100.0	31	15	US-10-005-305-69	Sequence 69, Appl	190	35	100.0	36	14	US-10-351-641-15	Sequence 15, Appl
118	35	100.0	31	15	US-10-005-305-199	Sequence 199, Appl	191	35	100.0	36	14	US-10-351-641-91	Sequence 91, Appl
119	35	100.0	32	14	US-10-351-641-743	Sequence 743, Appl	192	35	100.0	36	14	US-10-351-641-92	Sequence 92, Appl
120	35	100.0	32	14	US-10-351-641-798	Sequence 798, Appl	193	35	100.0	36	14	US-10-351-641-93	Sequence 93, Appl
121	35	100.0	32	14	US-10-351-641-802	Sequence 802, Appl	194	35	100.0	36	14	US-10-351-641-99	Sequence 99, Appl
122	35	100.0	32	15	US-10-005-305-30	Sequence 30, Appl	195	35	100.0	36	14	US-10-351-641-209	Sequence 209, Appl
123	35	100.0	32	15	US-10-005-305-63	Sequence 63, Appl	196	35	100.0	36	14	US-10-351-641-211	Sequence 211, Appl
124	35	100.0	32	15	US-10-005-305-68	Sequence 68, Appl	197	35	100.0	36	14	US-10-351-641-212	Sequence 212, Appl
125	35	100.0	33	14	US-10-351-641-61	Sequence 61, Appl	198	35	100.0	36	14	US-10-351-641-226	Sequence 226, Appl
126	35	100.0	33	14	US-10-351-641-639	Sequence 639, Appl	199	35	100.0	36	14	US-10-351-641-227	Sequence 227, Appl
127	35	100.0	33	14	US-10-351-641-797	Sequence 797, Appl	200	35	100.0	36	14	US-10-351-641-228	Sequence 228, Appl
128	35	100.0	33	14	US-10-351-641-801	Sequence 801, Appl	201	35	100.0	36	14	US-10-351-641-375	Sequence 375, Appl
129	35	100.0	33	15	US-10-005-305-31	Sequence 31, Appl	202	35	100.0	36	14	US-10-351-641-487	Sequence 497, Appl
130	35	100.0	33	15	US-10-005-305-64	Sequence 64, Appl	203	35	100.0	36	14	US-10-351-641-498	Sequence 498, Appl
131	35	100.0	33	15	US-10-005-305-198	Sequence 198, Appl	204	35	100.0	36	14	US-10-351-641-554	Sequence 549, Appl
132	35	100.0	34	14	US-10-351-641-741	Sequence 741, Appl	205	35	100.0	36	14	US-10-351-641-550	Sequence 550, Appl
133	35	100.0	34	14	US-10-351-641-796	Sequence 796, Appl	206	35	100.0	36	14	US-10-351-641-551	Sequence 551, Appl
134	35	100.0	34	14	US-10-351-641-800	Sequence 800, Appl	207	35	100.0	36	14	US-10-351-641-552	Sequence 552, Appl
135	35	100.0	34	15	US-10-005-305-32	Sequence 32, Appl	208	35	100.0	36	14	US-10-351-641-553	Sequence 553, Appl
136	35	100.0	34	15	US-10-005-305-65	Sequence 65, Appl	209	35	100.0	36	14	US-10-351-641-554	Sequence 554, Appl
137	35	100.0	34	15	US-10-252-136-17	Sequence 17, Appl	210	35	100.0	36	14	US-10-351-641-555	Sequence 555, Appl
138	35	100.0	35	14	US-10-351-641-48	Sequence 48, Appl	211	35	100.0	36	14	US-10-351-641-556	Sequence 556, Appl
139	35	100.0	35	14	US-10-351-641-376	Sequence 376, Appl	212	35	100.0	36	14	US-10-351-641-557	Sequence 557, Appl
140	35	100.0	35	14	US-10-351-641-544	Sequence 544, Appl	213	35	100.0	36	14	US-10-351-641-558	Sequence 558, Appl
141	35	100.0	35	14	US-10-351-641-636	Sequence 636, Appl	214	35	100.0	36	14	US-10-351-641-559	Sequence 559, Appl
142	35	100.0	35	14	US-10-351-641-638	Sequence 638, Appl	215	35	100.0	36	14	US-10-351-641-560	Sequence 560, Appl
143	35	100.0	35	14	US-10-351-641-638	Sequence 638, Appl	216	35	100.0	36	14	US-10-351-641-561	Sequence 561, Appl
144	35	100.0	35	14	US-10-351-641-795	Sequence 795, Appl	217	35	100.0	36	14	US-10-351-641-562	Sequence 562, Appl
145	35	100.0	35	14	US-10-351-641-799	Sequence 799, Appl	218	35	100.0	36	14	US-10-351-641-563	Sequence 563, Appl
146	35	100.0	35	14	US-10-351-641-1467	Sequence 1467, Appl	219	35	100.0	36	14	US-10-351-641-564	Sequence 564, Appl
147	35	100.0	35	15	US-10-005-305-33	Sequence 33, Appl	220	35	100.0	36	14	US-10-351-641-565	Sequence 565, Appl
148	35	100.0	35	15	US-10-005-305-66	Sequence 66, Appl	221	35	100.0	36	14	US-10-351-641-566	Sequence 566, Appl
149	35	100.0	36	9	US-09-796-202-10	Sequence 10, Appl	222	35	100.0	36	14	US-10-351-641-567	Sequence 567, Appl
150	35	100.0	36	9	US-09-779-451-5	Sequence 5, Appl	223	35	100.0	36	14	US-10-351-641-587	Sequence 587, Appl
151	35	100.0	36	9	US-09-779-451-47	Sequence 47, Appl	224	35	100.0	36	14	US-10-351-641-603	Sequence 603, Appl
152	35	100.0	36	9	US-09-779-451-50	Sequence 50, Appl	225	35	100.0	36	14	US-10-351-641-624	Sequence 624, Appl
153	35	100.0	36	9	US-09-779-451-56	Sequence 56, Appl	226	35	100.0	36	14	US-10-351-641-625	Sequence 625, Appl
154	35	100.0	36	9	US-09-912-824-1	Sequence 1, Appl	227	35	100.0	36	14	US-10-351-641-628	Sequence 628, Appl
155	35	100.0	36	9	US-09-834-628-1	Sequence 1, Appl	228	35	100.0	36	14	US-10-351-641-629	Sequence 629, Appl
156	35	100.0	36	9	US-09-854-816-1	Sequence 1, Appl	229	35	100.0	36	14	US-10-351-641-630	Sequence 630, Appl
157	35	100.0	36	9	US-09-854-816-108	Sequence 108, Appl	230	35	100.0	36	14	US-10-351-641-631	Sequence 631, Appl
158	35	100.0	36	9	US-09-874-475-16	Sequence 16, Appl	231	35	100.0	36	14	US-10-351-641-642	Sequence 642, Appl
159	35	100.0	36	10	US-09-493-346-1	Sequence 1, Appl	232	35	100.0	36	14	US-10-351-641-643	Sequence 643, Appl
160	35	100.0	36	14	US-10-116-797-1	Sequence 1, Appl	233	35	100.0	36	14	US-10-351-641-644	Sequence 644, Appl
161	35	100.0	36	14	US-10-252-136-1	Sequence 1, Appl	234	35	100.0	36	14	US-10-351-641-705	Sequence 705, Appl

235	35	100.0	36	14	US-10-351-641-719	Sequence 719, App	308	37	10	US-09-848-616-176	Sequence 176, App		
236	35	100.0	36	14	US-10-351-641-720	Sequence 720, App	309	37	14	US-10-347-562-1	Sequence 1, Appli		
237	35	100.0	36	14	US-10-351-641-721	Sequence 721, App	310	37	14	US-10-278-364A-8	Sequence 8, Appli		
238	35	100.0	36	14	US-10-351-641-728	Sequence 728, App	311	35	100.0	37	14	US-10-351-641-771	Sequence 771, App
239	35	100.0	36	14	US-10-351-641-729	Sequence 729, App	312	35	100.0	37	14	US-10-351-641-775	Sequence 775, App
240	35	100.0	36	14	US-10-351-641-730	Sequence 730, App	313	35	100.0	37	14	US-10-351-641-905	Sequence 905, App
241	35	100.0	36	14	US-10-351-641-731	Sequence 731, App	314	35	100.0	38	14	US-10-086-409A-3	Sequence 3, Appli
242	35	100.0	36	14	US-10-351-641-748	Sequence 748, App	315	35	100.0	38	14	US-10-351-641-762	Sequence 762, App
243	35	100.0	36	14	US-10-351-641-749	Sequence 749, App	316	35	100.0	38	14	US-10-351-641-772	Sequence 772, App
244	35	100.0	36	14	US-10-351-641-752	Sequence 752, App	317	35	100.0	38	14	US-10-351-641-776	Sequence 776, App
245	35	100.0	36	14	US-10-351-641-753	Sequence 753, App	318	35	100.0	38	14	US-10-351-641-780	Sequence 780, App
246	35	100.0	36	14	US-10-351-641-754	Sequence 754, App	319	35	100.0	38	14	US-10-351-641-1509	Sequence 1509, App
247	35	100.0	36	14	US-10-351-641-755	Sequence 755, App	320	35	100.0	39	14	US-10-252-136-30	Sequence 30, Appl
248	35	100.0	36	14	US-10-351-641-756	Sequence 756, App	321	35	100.0	39	14	US-10-351-641-517	Sequence 517, App
249	35	100.0	36	14	US-10-351-641-757	Sequence 757, App	322	35	100.0	39	14	US-10-351-641-602	Sequence 602, App
250	35	100.0	36	14	US-10-351-641-758	Sequence 758, App	323	35	100.0	39	14	US-10-351-641-632	Sequence 632, App
251	35	100.0	36	14	US-10-351-641-834	Sequence 834, App	324	35	100.0	39	14	US-10-351-641-773	Sequence 773, App
252	35	100.0	36	14	US-10-351-641-856	Sequence 856, App	325	35	100.0	39	14	US-10-351-641-777	Sequence 777, App
253	35	100.0	36	14	US-10-351-641-1051	Sequence 1051, App	326	35	100.0	39	14	US-10-351-641-1503	Sequence 1503, App
254	35	100.0	36	14	US-10-351-641-1076	Sequence 1076, App	327	35	100.0	40	9	US-09-854-816-113	Sequence 113, App
255	35	100.0	36	14	US-10-351-641-1121	Sequence 1121, App	328	35	100.0	40	14	US-10-351-641-774	Sequence 774, App
256	35	100.0	36	14	US-10-351-641-1161	Sequence 1161, App	329	35	100.0	40	14	US-10-351-641-778	Sequence 778, App
257	35	100.0	36	14	US-10-351-641-1248	Sequence 1248, App	330	35	100.0	40	14	US-10-351-641-781	Sequence 781, App
258	35	100.0	36	14	US-10-351-641-1249	Sequence 1249, App	331	35	100.0	40	15	US-10-283-403-13	Sequence 13, Appl
259	35	100.0	36	14	US-10-351-641-1250	Sequence 1250, App	332	35	100.0	41	15	US-10-351-641-640	Sequence 640, App
260	35	100.0	36	14	US-10-351-641-1251	Sequence 1251, App	333	35	100.0	41	16	US-10-231-494-16	Sequence 16, Appl
261	35	100.0	36	14	US-10-351-641-1356	Sequence 1356, App	334	35	100.0	42	14	US-10-351-641-746	Sequence 746, App
262	35	100.0	36	14	US-10-351-641-1357	Sequence 1357, App	335	35	100.0	44	14	US-10-351-641-999	Sequence 999, App
263	35	100.0	36	14	US-10-351-641-1358	Sequence 1358, App	336	35	100.0	44	15	US-10-283-403-11	Sequence 11, Appl
264	35	100.0	36	14	US-10-351-641-1359	Sequence 1359, App	337	35	100.0	45	14	US-10-086-409A-6	Sequence 6, Appli
265	35	100.0	36	14	US-10-351-641-1360	Sequence 1360, App	338	35	100.0	46	9	US-09-779-451-41	Sequence 41, Appl
266	35	100.0	36	14	US-10-351-641-1366	Sequence 1366, App	339	35	100.0	46	9	US-09-779-451-45	Sequence 45, Appl
267	35	100.0	36	14	US-10-351-641-1423	Sequence 1423, App	340	35	100.0	46	9	US-09-779-451-48	Sequence 48, Appl
268	35	100.0	36	14	US-10-351-641-1424	Sequence 1424, App	341	35	100.0	46	9	US-09-779-451-54	Sequence 54, Appl
269	35	100.0	36	14	US-10-351-641-1425	Sequence 1425, App	342	35	100.0	46	9	US-09-854-816-109	Sequence 109, App
270	35	100.0	36	14	US-10-351-641-1426	Sequence 1426, App	343	35	100.0	46	9	US-09-854-816-112	Sequence 112, App
271	35	100.0	36	14	US-10-351-641-1469	Sequence 1469, App	344	35	100.0	46	15	US-10-351-641-998	Sequence 998, App
272	35	100.0	36	14	US-10-351-641-1470	Sequence 1470, App	345	35	100.0	46	15	US-10-438-691-2	Sequence 2, Appli
273	35	100.0	36	14	US-10-351-641-1475	Sequence 1475, App	346	35	100.0	48	14	US-10-158-742A-15	Sequence 15, Appl
274	35	100.0	36	14	US-10-351-641-1476	Sequence 1476, App	347	35	100.0	48	14	US-10-351-641-45	Sequence 45, Appl
275	35	100.0	36	14	US-10-351-641-1477	Sequence 1477, App	348	35	100.0	48	14	US-10-351-641-547	Sequence 547, App
276	35	100.0	36	14	US-10-351-641-1478	Sequence 1478, App	349	35	100.0	48	14	US-10-252-136-11	Sequence 11, Appl
277	35	100.0	36	14	US-10-351-641-1479	Sequence 1479, App	350	35	100.0	50	14	US-10-351-641-959	Sequence 959, App
278	35	100.0	36	14	US-10-351-641-1482	Sequence 1482, App	351	35	100.0	52	14	US-10-158-742A-13	Sequence 13, Appl
279	35	100.0	36	14	US-10-351-641-1483	Sequence 1483, App	352	35	100.0	56	9	US-09-779-451-4	Sequence 4, Appli
280	35	100.0	36	14	US-10-351-641-1484	Sequence 1484, App	353	35	100.0	58	14	US-10-252-136-11	Sequence 11, Appl
281	35	100.0	36	14	US-10-351-641-1486	Sequence 1486, App	354	35	100.0	103	14	US-10-263-103-32	Sequence 32, Appl
282	35	100.0	36	14	US-10-351-641-1492	Sequence 1492, App	355	35	100.0	103	15	US-10-438-691-3	Sequence 3, Appli
283	35	100.0	36	14	US-10-351-641-1493	Sequence 1493, App	356	35	100.0	108	14	US-10-263-103-33	Sequence 33, Appl
284	35	100.0	36	14	US-10-351-641-1494	Sequence 1494, App	357	35	100.0	113	15	US-10-438-691-4	Sequence 4, Appli
285	35	100.0	36	14	US-10-351-641-1505	Sequence 1505, App	358	35	100.0	145	13	US-10-000-321-11	Sequence 11, Appl
286	35	100.0	36	14	US-10-351-641-1506	Sequence 1506, App	359	35	100.0	177	14	US-10-040-349B-2	Sequence 2, Appli
287	35	100.0	36	14	US-10-351-641-1507	Sequence 1507, App	360	35	100.0	189	9	US-09-854-816-100	Sequence 100, App
288	35	100.0	36	14	US-10-351-641-1508	Sequence 1508, App	361	35	100.0	198	9	US-09-854-816-86	Sequence 86, Appl
289	35	100.0	36	14	US-10-351-641-1510	Sequence 1510, App	362	35	100.0	198	9	US-09-854-816-87	Sequence 87, Appl
290	35	100.0	36	14	US-10-351-641-1511	Sequence 1511, App	363	35	100.0	198	9	US-09-854-816-88	Sequence 88, Appl
291	35	100.0	36	14	US-10-351-641-1512	Sequence 1512, App	364	35	100.0	198	9	US-09-854-816-89	Sequence 89, Appl
292	35	100.0	36	14	US-10-351-641-1514	Sequence 1514, App	365	35	100.0	198	9	US-09-854-816-90	Sequence 90, Appl
293	35	100.0	36	14	US-10-351-641-1515	Sequence 1515, App	366	35	100.0	198	9	US-09-854-816-99	Sequence 99, Appl
294	35	100.0	36	14	US-10-351-641-1516	Sequence 1516, App	367	35	100.0	198	9	US-09-854-816-101	Sequence 101, App
295	35	100.0	36	14	US-10-351-641-1517	Sequence 1517, App	368	35	100.0	198	9	US-10-263-103-25	Sequence 25, Appl
296	35	100.0	36	14	US-10-351-641-1518	Sequence 1518, App	369	35	100.0	200	14	US-10-438-691-8	Sequence 8, Appli
297	35	100.0	36	14	US-10-351-641-1519	Sequence 1519, App	370	35	100.0	200	15	US-10-059-271-84	Sequence 84, Appl
298	35	100.0	36	14	US-10-351-641-1520	Sequence 1520, App	371	35	100.0	221	14	US-10-059-271-81	Sequence 81, Appl
299	35	100.0	36	14	US-10-351-641-1749	Sequence 1749, App	372	35	100.0	232	14	US-09-854-816-50	Sequence 50, Appl
300	35	100.0	36	14	US-10-351-641-1750	Sequence 1750, App	373	35	100.0	233	9	US-10-059-271-97	Sequence 97, Appl
301	35	100.0	36	14	US-10-351-641-1751	Sequence 1751, App	374	35	100.0	254	14	US-10-059-271-82	Sequence 82, Appl
302	35	100.0	36	15	US-10-005-305-34	Sequence 34, Appl	375	35	100.0	256	14	US-10-059-271-97	Sequence 97, Appl
303	35	100.0	36	15	US-10-005-305-67	Sequence 67, Appl	376	35	100.0	267	9	US-09-854-816-15	Sequence 15, Appl
304	35	100.0	36	15	US-10-005-305-197	Sequence 197, App	377	35	100.0	267	9	US-09-854-816-38	Sequence 38, Appl
305	35	100.0	36	15	US-10-378-094-17	Sequence 17, Appl	378	35	100.0	268	9	US-09-854-816-7	Sequence 7, Appli
306	35	100.0	36	15	US-10-420-194-1233	Sequence 1233, App	379	35	100.0	268	9		
307	35	100.0	36	16	US-10-231-494-14	Sequence 14, Appl	380	35	100.0				

381	35	100.0	268	9	US-09-854-816-8	Sequence 8, Appl	454	32	91.4	36	14	US-10-351-641-95	Sequence 95, Appl
382	35	100.0	268	9	US-09-854-816-9	Sequence 9, Appl	455	32	91.4	36	14	US-10-351-641-1223	Sequence 1223, Ap
383	35	100.0	268	9	US-09-854-816-10	Sequence 10, Appl	456	32	91.4	36	14	US-10-351-641-1361	Sequence 1361, Ap
384	35	100.0	268	9	US-09-854-816-11	Sequence 11, Appl	457	32	91.4	36	14	US-10-351-641-1444	Sequence 1444, Ap
385	35	100.0	268	9	US-09-854-816-12	Sequence 12, Appl	458	32	91.4	36	14	US-10-351-641-1449	Sequence 1449, Ap
386	35	100.0	268	9	US-09-854-816-13	Sequence 13, Appl	459	32	91.4	36	14	US-10-351-641-1450	Sequence 1450, Ap
387	35	100.0	268	9	US-09-854-816-14	Sequence 14, Appl	460	32	91.4	36	14	US-10-351-641-1447	Sequence 1447, Ap
388	35	100.0	268	9	US-09-854-816-15	Sequence 15, Appl	461	32	91.4	40	14	US-10-351-641-1448	Sequence 1448, Ap
389	35	100.0	268	9	US-09-854-816-16	Sequence 16, Appl	462	32	91.4	198	9	US-09-854-816-85	Sequence 85, Appl
390	35	100.0	268	9	US-09-854-816-17	Sequence 17, Appl	463	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
391	35	100.0	268	9	US-09-854-816-18	Sequence 18, Appl	464	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
392	35	100.0	268	9	US-09-854-816-19	Sequence 19, Appl	465	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
393	35	100.0	268	9	US-09-854-816-20	Sequence 20, Appl	466	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
394	35	100.0	268	9	US-09-854-816-21	Sequence 21, Appl	467	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
395	35	100.0	268	9	US-09-854-816-22	Sequence 22, Appl	468	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
396	35	100.0	268	9	US-09-854-816-23	Sequence 23, Appl	469	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
397	35	100.0	268	9	US-09-854-816-24	Sequence 24, Appl	470	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
398	35	100.0	268	9	US-09-854-816-25	Sequence 25, Appl	471	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
399	35	100.0	268	9	US-09-854-816-26	Sequence 26, Appl	472	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
400	35	100.0	268	9	US-09-854-816-27	Sequence 27, Appl	473	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
401	35	100.0	268	9	US-09-854-816-28	Sequence 28, Appl	474	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
402	35	100.0	268	9	US-09-854-816-29	Sequence 29, Appl	475	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
403	35	100.0	268	9	US-09-854-816-30	Sequence 30, Appl	476	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
404	35	100.0	268	9	US-09-854-816-31	Sequence 31, Appl	477	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
405	35	100.0	268	9	US-09-854-816-32	Sequence 32, Appl	478	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
406	35	100.0	268	9	US-09-854-816-33	Sequence 33, Appl	479	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
407	35	100.0	268	9	US-09-854-816-34	Sequence 34, Appl	480	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
408	35	100.0	268	9	US-09-854-816-35	Sequence 35, Appl	481	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
409	35	100.0	268	9	US-09-854-816-36	Sequence 36, Appl	482	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
410	35	100.0	268	9	US-09-854-816-37	Sequence 37, Appl	483	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
411	35	100.0	268	9	US-09-854-816-38	Sequence 38, Appl	484	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
412	35	100.0	268	9	US-09-854-816-39	Sequence 39, Appl	485	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
413	35	100.0	268	9	US-09-854-816-40	Sequence 40, Appl	486	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
414	35	100.0	268	9	US-09-854-816-41	Sequence 41, Appl	487	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
415	35	100.0	268	9	US-09-854-816-42	Sequence 42, Appl	488	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
416	35	100.0	268	9	US-09-854-816-43	Sequence 43, Appl	489	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
417	35	100.0	268	9	US-09-854-816-44	Sequence 44, Appl	490	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
418	35	100.0	268	9	US-09-854-816-45	Sequence 45, Appl	491	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
419	35	100.0	268	9	US-09-854-816-46	Sequence 46, Appl	492	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
420	35	100.0	268	9	US-09-854-816-47	Sequence 47, Appl	493	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
421	35	100.0	268	9	US-09-854-816-48	Sequence 48, Appl	494	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
422	35	100.0	268	9	US-09-854-816-49	Sequence 49, Appl	495	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
423	35	100.0	268	9	US-09-854-816-50	Sequence 50, Appl	496	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
424	35	100.0	268	9	US-09-854-816-51	Sequence 51, Appl	497	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
425	35	100.0	268	9	US-09-854-816-52	Sequence 52, Appl	498	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
426	35	100.0	268	9	US-09-854-816-53	Sequence 53, Appl	499	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
427	35	100.0	268	9	US-09-854-816-54	Sequence 54, Appl	500	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
428	35	100.0	268	9	US-09-854-816-55	Sequence 55, Appl							
429	35	100.0	268	9	US-09-854-816-56	Sequence 56, Appl							
430	35	100.0	268	9	US-09-854-816-57	Sequence 57, Appl							
431	35	100.0	268	9	US-09-854-816-58	Sequence 58, Appl							
432	35	100.0	268	9	US-09-854-816-59	Sequence 59, Appl							
433	35	100.0	268	9	US-09-854-816-60	Sequence 60, Appl							
434	35	100.0	268	9	US-09-854-816-61	Sequence 61, Appl							
435	35	100.0	268	9	US-09-854-816-62	Sequence 62, Appl							
436	35	100.0	268	9	US-09-854-816-63	Sequence 63, Appl							
437	35	100.0	268	9	US-09-854-816-64	Sequence 64, Appl							
438	35	100.0	268	9	US-09-854-816-65	Sequence 65, Appl							
439	35	100.0	268	9	US-09-854-816-66	Sequence 66, Appl							
440	35	100.0	268	9	US-09-854-816-67	Sequence 67, Appl							
441	35	100.0	268	9	US-09-854-816-68	Sequence 68, Appl							
442	35	100.0	268	9	US-09-854-816-69	Sequence 69, Appl							
443	35	100.0	268	9	US-09-854-816-70	Sequence 70, Appl							
444	35	100.0	268	9	US-09-854-816-71	Sequence 71, Appl							
445	35	100.0	268	9	US-09-854-816-72	Sequence 72, Appl							
446	35	100.0	268	9	US-09-854-816-73	Sequence 73, Appl							
447	35	100.0	268	9	US-09-854-816-74	Sequence 74, Appl							
448	35	100.0	268	9	US-09-854-816-75	Sequence 75, Appl							
449	35	100.0	268	9	US-09-854-816-76	Sequence 76, Appl							
450	35	100.0	268	9	US-09-854-816-77	Sequence 77, Appl							
451	35	100.0	268	9	US-09-854-816-78	Sequence 78, Appl							
452	35	100.0	268	9	US-09-854-816-79	Sequence 79, Appl							
453	35	100.0	268	9	US-09-854-816-80	Sequence 80, Appl							

RESULT 1

US-09-873-459A-4

; Sequence 4, Application US/09873459A

; Patent No. US20020064533A1

; GENERAL INFORMATION:

; APPLICANT: Murray, Kenneth

; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC

; FILE REFERENCE: A067 CIP

; CURRENT APPLICATION NUMBER: US/09/873,459A

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: PCT/US99/28755

; PRIOR FILING DATE: 1999-12-03

; PRIOR APPLICATION NUMBER: 60/110,911

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus

ALIGNMENTS

US-09-873-459A-4.

Query Match 100.0%; Score 35; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 2

US-10-041-414-7

; Sequence 7, Application US/10041414
; Publication No. US20030087225A1

GENERAL INFORMATION:

; APPLICANT: SHIVER, JOHN W.
; DAVIES, MARY ELLEN

FREED, DANIEL C.

LIU, MARGARET A.

PERRY, HELEN C.

; TITLE OF INVENTION: SYNTHETIC HIV ENV GENES

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: J. MARK HAND - MERCK & CO., INC.

STREET: 126 E. LINCOLN AVE., - P.O. BOX 2000

CITY: RAHWAY

STATE: NEW JERSEY

COUNTRY: US

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/041,414

FILING DATE: 08-May-2002

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/802,368

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: HAND, J. MARK

REGISTRATION NUMBER: 36,545

REFERENCE/DOCKET NUMBER: 19643

TELEPHONE: 732-594-3905

TELEFAX: 732-594-4720

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-041-414-7

Query Match 100.0%; Score 35; DB 14; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.1e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6

| | | | |

Db 1 ELDKWA 6

RESULT 3

US-10-024-329-2

; Sequence 2, Application US/10024329

; Publication No. US20030157063A1

GENERAL INFORMATION:

APPLICANT: SANHADJI, Kamel

APPLICANT: TOURAINE, Jean-Louis

APPLICANT: LEROY, Pierre

APPLICANT: MEHTALI, Majid

TITLE OF INVENTION: Gene therapy using anti-gp41 antibody and cd4 immunoadhesin

FILE REFERENCE: 109993

CURRENT APPLICATION NUMBER: US/10/024,329

CURRENT FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 6

TYPE: PRT

ORGANISM: HIV-1 gp41 epitope

US-10-024-329-2

Query Match 100.0%; Score 35; DB 14; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.1e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6

| | | | |

Db 1 ELDKWA 6

RESULT 4

US-10-448-546-4

; Sequence 4, Application US/10448546

; Publication No. US20030198649A1

GENERAL INFORMATION:

APPLICANT: Murray, Kenneth

TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC

TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS

FILE REFERENCE: A067 CIP CON DIV 1

CURRENT APPLICATION NUMBER: US/10/448,546

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: US/09/873,459

PRIOR APPLICATION NUMBER: 2001-06-04

PRIOR APPLICATION NUMBER: PCT/US99/28755

PRIOR FILING DATE: 1999-12-03

PRIOR APPLICATION NUMBER: 60/110,911

PRIOR FILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 6

TYPE: PRT

ORGANISM: Human immunodeficiency virus

US-10-448-546-4

Query Match 100.0%; Score 35; DB 14; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.1e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6

| | | | |

Db 1 ELDKWA 6

RESULT 5

US-10-283-403-12

; Sequence 12, Application US/10283403

; Publication No. US20030219451A1

GENERAL INFORMATION:

APPLICANT: Kim, Peter S.

APPLICANT: Sia, Samuel K.

TITLE OF INVENTION: Stable Helical C Peptides and Uses

TITLE OF INVENTION: Therefor

FILE REFERENCE: 0399.2035-002

CURRENT APPLICATION NUMBER: US/10/283,403

CURRENT FILING DATE: 2002-10-29

; PRIOR APPLICATION NUMBER: US 60/350,099
 ; PRIOR FILING DATE: 2001-10-29
 ; PRIOR APPLICATION NUMBER: US 60/334,528
 ; PRIOR FILING DATE: 2001-11-30
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Core epitope for the 2F5 monoclonal antibody
 US-10-283-403-12

Query Match 100.0%; Score 35; DB 15; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.1e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
 Db 1 ELDKWA 6

RESULT 6
 US-10-369-121-53
 ; Sequence 53, Application US/10369121
 ; Publication No. US20030229214A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SHIVER, JOHN W.
 ; LIU, MARGARET A.
 ; PERRY, HELEN C.
 ; DAVIES, MARY-ELLEN M.
 ; FREED, DANIEL C.

; TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES
 ; NUMBER OF SEQUENCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
 ; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
 ; CITY: RAHWAY
 ; STATE: NEW JERSEY
 ; COUNTRY: US
 ; ZIP: 07065-0907

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/369,121
 ; FILING DATE: 17-Feb-2003
 ; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/340,798A
 ; FILING DATE: 28-Jun-1999
 ; APPLICATION NUMBER: US/08/877,418
 ; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:
 ; NAME: HAND, J. MARK
 ; REGISTRATION NUMBER: 36,545
 ; REFERENCE/DOCKET NUMBER: 19729Y
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 908-594-3905
 ; TELEFAX: 908-594-4720

; INFORMATION FOR SEQ ID NO: 53:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
 US-10-369-121-53

Query Match 100.0%; Score 35; DB 15; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.1e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
 Db 1 ELDKWA 6

RESULT 7
 US-09-873-459A-2
 ; Sequence 2, Application US/09873459A
 ; Patent No. US20020064533A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murray, Kenneth
 ; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
 ; FILE REFERENCE: A067 CIP
 ; CURRENT FILING DATE: 2001-09-17
 ; CURRENT APPLICATION NUMBER: PCT/US99/28755
 ; PRIOR FILING DATE: 1999-12-03
 ; PRIOR APPLICATION NUMBER: 60/110,911
 ; PRIOR FILING DATE: 1998-12-04
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-09-873-459A-2

Query Match 100.0%; Score 35; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.1e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
 Db 1 ELDKWA 6

RESULT 8
 US-10-448-546-2
 ; Sequence 2, Application US/10448546
 ; Publication No. US20030198649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murray, Kenneth

; TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
 ; FILE REFERENCE: A067 CIP CON DIV 1
 ; CURRENT APPLICATION NUMBER: US/10/448,546
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: US/09/873,459
 ; PRIOR FILING DATE: 2001-06-04
 ; PRIOR APPLICATION NUMBER: PCT/US99/28755
 ; PRIOR FILING DATE: 1999-12-03
 ; PRIOR APPLICATION NUMBER: 60/110,911
 ; PRIOR FILING DATE: 1998-12-04
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-448-546-2

Query Match 100.0%; Score 35; DB 14; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.1e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
 Db 1 ELDKWA 6

```

; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-31

Query Match      100.0%; Score 35; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      1 ELDKWA 6
        |||||

RESULT 12
US-10-200-708-404
; Sequence 404, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 404
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-404

Query Match      100.0%; Score 35; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      2 ELDKWA 7
        |||||

RESULT 13
US-10-200-708-456
; Sequence 456, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; FILE REFERENCE: 17999-001

```

```

; CURRENT APPLICATION NUMBER: US/09931325A
; Publication No. US20030054337A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/83503 ICC-103.1
; CURRENT APPLICATION NUMBER: US/09/931,325A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US/09/930,915A
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-931-325A-132

Query Match      100.0%; Score 35; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      3 ELDKWA 8
        |||||

RESULT 10
US-09-930-915A-173
; Sequence 173, Application US/09930915A
; Publication No. US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; TITLE OF INVENTION: STABILITY
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 173
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-930-915A-173

Query Match      100.0%; Score 35; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      3 ELDKWA 8
        |||||

RESULT 11
US-10-200-708-31
; Sequence 31, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001

```

; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 456
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-456

Query Match 100.0%; Score 35; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7
|||||

RESULT 14

US-10-200-708-477
; Sequence 477, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 477
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-477

Query Match 100.0%; Score 35; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7
|||||

RESULT 15

US-10-351-641-219
; Sequence 219, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M. D.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641

; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 219
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-219

Query Match 100.0%; Score 35; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 16

US-10-005-305-43
; Sequence 43, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-43

Query Match 100.0%; Score 35; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 17

US-10-005-305-88
; Sequence 88, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1


```
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
; US-10-005-305-88

Query Match      100.0%; Score 35; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 1 ELDKWA 6

RESULT 18
US-10-252-136-22
; Sequence 22, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-10-252-136-22

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 19
US-10-252-136-23
; Sequence 23, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-10-252-136-23

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 20
US-10-252-136-24
; Sequence 24, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-10-252-136-24

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 21
US-10-252-136-25
; Sequence 25, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-10-252-136-25

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7
```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
Db 2 ELDKWA 7

RESULT 22
US-10-252-136-26
; Sequence 26, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-26

Query Match 100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
Db 2 ELDKWA 7

RESULT 23
US-10-351-641-218
; Sequence 218, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 218
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-218

Query Match 100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
Db 2 ELDKWA 7

RESULT 24
US-10-351-641-267
; Sequence 267, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 267
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-267

Query Match 100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
Db 2 ELDKWA 7

RESULT 25
US-10-351-641-268
; Sequence 268, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 268
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-351-641-268

Query Match 100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-268

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7

RESULT 26
US-10-351-641-269
; Sequence 269, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 269
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-269

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7

RESULT 27
US-10-351-641-270
; Sequence 270, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
```

```
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 270
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-270

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7

RESULT 28
US-10-351-641-530
; Sequence 530, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-530

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7

RESULT 29
US-10-351-641-531
; Sequence 531, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
```

```
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-531

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 30
US-10-005-305-44
; Sequence 44, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-44

Query Match      100.0%; Score 35; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 31
US-10-005-305-87
; Sequence 87, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-87

Query Match      100.0%; Score 35; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 32
US-09-931-325A-133
; Sequence 133, Application US/09931325A
; Publication No. US20030054337A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/83503 ICC-103.1
; CURRENT APPLICATION NUMBER: US/09/931,325A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: USSN NOT YET ASSIGNED
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-931-325A-133

Query Match      100.0%; Score 35; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 6 ELDKWA 11

RESULT 33
US-09-930-915A-174
; Sequence 174, Application US/09930915A
; Publication No. US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; TITLE OF INVENTION: STABILITY
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-930-915A-174

Query Match      100.0%; Score 35; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      6 ELDKWA 11

RESULT 34
US-10-351-641-217
; Sequence 217, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 217
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Core polypeptide
US-10-351-641-217

Query Match      100.0%; Score 35; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      3 ELDKWA 8

RESULT 35
US-10-351-641-229
; Sequence 229, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 217
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Core polypeptide
US-10-351-641-217

Query Match      100.0%; Score 35; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      3 ELDKWA 8

RESULT 36
US-10-005-305-45
; Sequence 45, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DPI78 AND T21/DPI07 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-45

Query Match      100.0%; Score 35; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      3 ELDKWA 8

RESULT 37
US-10-005-305-86
; Sequence 86, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DPI78 AND T21/DPI07 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
```

```
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-86

Query Match          100.0%; Score 35; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 3 ELDKWA 8

RESULT 38
US-09-810-310-41
; Sequence 41, Application US/09810310
; Patent No. US20020044948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Bezofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIIGEN
US-09-810-310-41

Query Match          100.0%; Score 35; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 6 ELDKWA 11

RESULT 39
US-10-252-136-19
; Sequence 19, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-19

Query Match          100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 3 ELDKWA 8

RESULT 40
US-10-252-136-20
; Sequence 20, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-20

Query Match          100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 3 ELDKWA 8

RESULT 41
US-10-252-136-21
; Sequence 21, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-21

Query Match          100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1  ELDKWA 6
      |||||
Db      3  ELDKWA 8

RESULT 42
US-10-351-641-216
; Sequence 216, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351.641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 216
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-216

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELDKWA 6
      |||||
Db      4  ELDKWA 9

RESULT 43
US-10-351-641-372
; Sequence 372, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351.641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-372

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELDKWA 6
      |||||
Db      3  ELDKWA 8

RESULT 44
US-10-351-641-373
; Sequence 373, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351.641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-373

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELDKWA 6
      |||||
Db      3  ELDKWA 8

RESULT 45
US-10-351-641-374
; Sequence 374, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351.641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-374
```

```
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-372

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELDKWA 6
      |||||
Db      3  ELDKWA 8

RESULT 44
US-10-351-641-373
; Sequence 373, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351.641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-373

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELDKWA 6
      |||||
Db      3  ELDKWA 8

RESULT 45
US-10-351-641-374
; Sequence 374, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351.641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-374
```

```
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-374

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
        |||||
Db      3 ELDKWA 8

RESULT 46
US-10-351-641-513
; Sequence 513, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 513
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-513

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
        |||||
Db      3 ELDKWA 8

RESULT 47
US-10-351-641-514
; Sequence 514, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 514
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-514

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
        |||||
Db      3 ELDKWA 8

RESULT 48
US-10-351-641-515
; Sequence 515, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 515
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-515

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
        |||||
Db      3 ELDKWA 8

RESULT 49
US-10-351-641-792
; Sequence 792, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
```


; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 792
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-792

Query Match 100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 4 ELDKWA 9

RESULT 50
US-10-005-305-46
; Sequence 46, Application US/10005305
; Publication No. US20030203941A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-46

Query Match 100.0%; Score 35; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 4 ELDKWA 9

Search completed: March 16, 2004, 09:19:33
Job time : 35 secs

THIS PAGE BLANK (USPTO)